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Statistics: Mean 11.935; Variance 4.909; scale 2.431

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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> Description: Perfect Score: N.A. Sequence:

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514334 seqs, 179763086 bases x 2

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

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98:EST91 99:EST92 100:EST93 101:EST94 102:EST95
103:EST96 104:EST97 105:EST98 106:EST99 107:EST100
108:EST101 109:qnEST1 110:qnEST2 111:qnEST3 112:qnEST4
113:qnEST5 114:qnEST6 115:qnEST7 116:qnEST8 117:qnEST9
118:qnEST10 119:qnEST11 120:qnEST12 121:qnEST13
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Database:

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HS587267 standard; RNA; EST; 642 BP.

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Db 419 gttaatcccagctactcaggaggctaaggcaggagaattgcttgaacctgggangcggag 478	Db 479 gttatgggtgagccaggtcgtgccattgcactccagcttgggcaacaaaagcgaactcc 538 	Db 539 catctcaaaaaagag 554 	RESULT 2 LOCUS N26587 642 bp mRNA EST 29-DEC-1995 DEFINITION yx91e07.sl Homo sapiens cDNA clone 269124 3' similar to contains Alu repetitive element;			CANANALOR GAPIENS  Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  Euvterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Entheria: Archonta: Primates: Catarthin; Hominidae: Homo.	REFERENCE 1 (bases 1 to 642) AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Kucaba, T., Ley, M., Lennon, G., Marra, M., Darense, J. Rifkin, T. Rarier, M., Tan, F.	Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. TITLE The WashU-Merck EST Project JOURNAL Unpublished (1995)	COMMENT Contact: Wilson RK WashU-Merck EST Project WashInton University School of Medicine	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Fmail: est@waten.wistl.edu	High quality sequence stops: 385 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@imaqe.llnl.qov) for further information.	NCBI gi: 1140935  FEATURES Location/Qualifiers  source 1642 /organism="Homo sapiens"
N26587; 30-DEC-1995 (Rel. 46, Created) 30-DEC-1995 (Rel. 46, Last updated, Version 1) yx91e07.sl Homo sapiens CDNA clone 269124 3' similar to contains		neria; Eucheria; Frimaces; Hapiochini; Cacafrinini; Nominidae. [1] 1-642 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfinn T., Soares M., Tan F.,	Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project", Unpublished. Contact: Wilson RK WashU-Merck EST Project Washington University Cohtact: Wallson RK WashU-Merck EST Project Washington University	School of Medicine 4444 Forest Park Farkady, Box 8001, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Faxilises 18 Faxilises 1	source 1642 /organism="Homo sapiens" /clone="269124" /note="human" mRNA <1>642 Sequence 642 BP; 182 A; 135 C; 152 G; 166 T; 7 other;	Query Match 33.3%; Score 519; DB 134; Length 642; Best Local Similarity 97.8%; Pred. No. 0.00e+00; Matches 544; Conservative 0; Mismatches 9; Indels 3; Gaps 3;	l gaatototgatootttatgatttottotgoacattottggagaggattgggaaco-a 59 	60 agagagctaaattgccataggtacatttaaggcagtacacaggcatcagcactaaggcag 119 	120 tacatagtagcttttacttatttaaatccttctaccaatttctggtttagtagaaaatac 179 	180 ttgtcattagttagaatagcattgaagcttgaagtgaaatgtaattagactgcgttatat 239 	240 gtcttacctaagatataggatccagccaggcgtggtggctcacgc-tgtaattccagcac 298 	299 tttgggaggctgaggcgagatcacctgaggtcaggatttgagaccagcctgaccaa 358

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foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, 10; This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. gagaagatgctcactcatctatggttaccccaagaaggggcacggccactcttacacca 121 181 61 GAGAAGATGCTCACTTCATCTATGCTTACCCCAAGAAGGGGCACGCCACCTCTTACACCA 120 182 tcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaaagtcttc 241 1 (bases 1 to 593)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and 2 agcagacagaggactctcattaaggaaggtgtcctgtgccctgacctacaagatgccaa 61 Gaps 122 cggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtcttactgctca Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 0; Mismatches 10; Indels 10; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 593; 5 others Score 488; DB 113; Pred. No. 0.00e+00; Washington University School of Medicine 146 t /organism="Homo sapiens" /clone="263710" /note="human" High quality sequence stops: 414 Source: IMAGE Consortium, LLNL NCBI gi: 1137920 Location/Qualifiers 6 Email: est@watson.wustl.edu Wilson, R. The WashU-Merck EST Project 137 Contact: Wilson RK WashU-Merck EST Project uery Match 31.3%; est Local Similarity 96.5%; 140 c atches 555; Conservative Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 <1..>593 1..593Homo sapiens 165 source mRNA E COUNT RGANISM TTLE OURNAL MENT UTHORS 62 ERENCE

181 TCGCTGTTGGTATTGTAGAAGACGAAATGGATACAGAGCCTTGATGGATAAAAGTCTTC 240

241 ATGTTGGCACTCAATGTGCCTTAACAAGAAGATGCCCACAAGAAGGGTTTGATCATCATCGG 300

302 acagcaaagtgtctctccaagagaaaaactgtgaacctgtggttcccaatgctccacctg 361

242 atgttggcactcaatgtgccttaacaagaagatgcccacaagaagggtttgatcatcggg 301

61 GAGAAGATGCTCACTTCATCTATGGTTACCCCAAGAAGGGGCACGGCCACTCTTACACCA 120

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62 gagaagatgeteaetteatetatggttaceceaagaaggggeaeggeeaetettaeaeea 121

1 AGCAGACAGAGGACTCTCATTAAGGAAGGTGTCCTGTGCCCTGACCCTACAAGATGCCAA 60

2 agcagacagaggactctcattaaggaaggtgtcctgtgcctgaccctacaagatgccaa

10;

Gaps 61

0; Mismatches 10; Indels 10;

Score 488; DB 136; Length 593; Pred. No. 0.00e+00;

31.3%; 96.5%;

Best Local Similarity 96.5%; Matches 555; Conservative

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Query Match

<1..>593
BP; 165 A; 140 C; 137 G; 146 T; 5 other;

Sequence 593

mRNA

/organism="Homo sapiens"

source

/clone="263710" /note="human"

Location/Qualifiers

information. NCBI gi: 1137920

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Harsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project";

est@watson.wustl.edu High quality sequence stops: 414 Source: IMAGE Consortium, LIAL This clone is available royalty-free through LIAL, contact the IMAGE Consortium (info@image.llnl.gov) for further

School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louiê, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

Contact: Wilson RK WashU-Merck EST Project Washington University

Unpublished

GACACCTG-AGACATGCTGAAATTATTCTC-TCACACTTTTGCTTGAATTTAATACAGA 478 301 ACAGGAAAGTGTCTCTTCAAGAGAAAACTGTGAACCTGTGGTTCCCAATGCTCCACCTG 360 cttatgagaaactctctgcagaacagtcaccaccaccttattcaccttaagagccagcga 421 gacacctggagacatgctgaaattatttctcctcacacttttgcttgaatttaatacagg 481 ccatctaatggttctccctttgggaatgggtgtaggnaaaatgncaacccactctaatna 541 Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Mammalia; Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Version 1) yx35a12.r1 Homo sapiens cDNA clone 263710 5' ВЪ. 29-DEC-1995 (Rel. 46, Created) 29-DEC-1995 (Rel. 46, Last updated, HS770262 standard; RNA; EST; 593 Homo sapiens (human) 1 - 593362 422 421 482 479 g 셤 ò à ⋧ 임 ò 용 δ

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S 4; ywllh07.s1 Homo sapiens cDNA clone 251965 3' similar to contains Alu repetitive element;. TTT-GGGAGGCTGAGGCGGGCAGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGACCA 1164 ttgtcattagttagaatagcattgagccttgaagtgaaatgtaattagactgcgttatat 243 304 ttttgggaggctgaggcgggcagatcacctgaggtcaggagtttgagaccagcctgacca 363 64 agagagctaaattgccataggtacatttaaggcagtacacaggcatcagcactaaggcag 123 124 tacatagtagcttttacttatttaaatccttctaccaatttctggtttagtagaaaatac 183 364 acatgggngaaaccccgnctctactaaaactacaaaattagtcaggcanagtggcgcacn 423 4 gaatetetgateetttatgatttettetgeacattettgtgagagggatttgggaaceca 63 Gaps 12-DEC-1995 4; Score 482; DB 134; Length 522; Pred. No. 0.00e+00; Indels BP; 143 A; 109 C; 128 G; 135 T; 7 other; EST 8 0; Mismatches /organism="Homo sapiens" /clone="251965" /note="human" PRNA 522 bp Query Match 30.9%; Best Local Similarity 97.7%; Matches 507; Conservative

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ACCESSION KEYWORDS SOURCE

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Albino

S.	ORGANISM	Homo sapiens
		Deuterostomia; Chordata; Vertebrata; Chathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFE AU	REFERENCE AUTHORS	<pre>i (bases I to 521) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Ellow</pre>
TITLE JOURN COMMENT	TITLE JOURNAL MMENT	TiteUnity. The WashU-Merck EST Project Unpublished (1995)
		Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine HA44 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1808
		Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 313 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES sou	URES source	NCBI gi: 1118395 Location/Qualifiers 1522
BASE COORIGIN	mRNA COUNT IN	/organism="Homo sapien /clone="251965" /note="human" <1552 143 a 109 c 128 g
A Be	Query Match Best Local Matches 5	Query Match 30.9%; Score 482; DB 111; Length 522; Best Local Similarity 97.7%; Pred. No. 0.00e+00; Matches 507; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
QQ	4	gaatctctgatcctttatgatttcttctgcacattcttgtggagggatttgggaacca 63
g,	1522	GAATOTCTGATCCTTTATGATTTCTTCTGCACATTCTTGTGAGGGATTTGGGAACCCA 1463
q	64	agagagctaaattgccataggtacatttaaggcagtacacaggcatcagcactaaggcag 123
g,	1462	AGAGAGCTAAATTGCCATAGGTACATTTAAGGCAGTACACAGGCATCAGCACTAAGGCAG 1403
QC	124	tacatagtagcttttacttatttaaatccttctaccaatttctggtttagtagaaatac 183
ç	1402	TACATAGTAGCTTTTACTTATTTAATCCTTCTACCAATTTCTGGTTTAGTAGAAATAC 1343
QQ	184	ttgtcattagttagaatagcattgagccttgaaqtgaaatgtaattagactgcgttatat 243
g,	1342	ITCTCATTAGTTAGAATAGCATTGAGCCTTGAAGTGAAATCTAATTAGACTGCGTTATAT 1283
q	244	gtcttacctaagatataggatccagccaggcgtggtggtgccagcctgtaattccagcac 303
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aggttatggngagcccagatcgcggccattgcactccag 521

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540 bp

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DEFINITION

q1118383

ACCESSION

KEYWORDS SOURCE

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62 Gaps

Homo sapiens

ORGANISM

Albino.

Washington University School of Medicine

WashU-Merck EST Project

Contact: Wilson RK Unpublished (1995)

The WashU-Merck EST Project

TITLE JOURNAL

COMMENT

Wilson, R.

AUTHORS

REFERENCE

High quality sequence stops: 377 Source: IMAGE Consortium, LLNL

This

Email: est@watson.wustl.edu

/organism="Homo saplens"

/clone="251941" /note="human"

Location/Qualifiers

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Bource

FEATURES

EST. human clone=263806 primer=ml3 -40 forward library=Soares melanocyte 1522 GAATCTCTGATCCTTTATGATTTCTTCTGCACATTCTTGTGAGGGGATTTGGGAACCCA 1463 1402 TACATAGTAGCTTTTACTTATTTAAATCCTTCTACCAATTTCTGGTTTAGTAGAAAATAC 1343 1342 ITGTCATTAGTTAGAATAGCATTGAGCCTTGAAGTGAAATGTAATTAGACTGCGTTATAT 1283 1282 GTCTTACCTAAGATATAGGATCCAGCCAGGCGTGGTGGCTCACGCCTGTAATTCCAGCAC 1223 1104 CCTGTAATCCCAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCTTGAACCTGGG--AGGC 1047 123 tacatagtagcttttacttatttaaatccttctaccaatttctggtttagtagaaatac 182 243 gtcttacctaagatataggatccagccaggcgtggtggctcacgcctgtaattccagcac 302 303 tttgggaggctgaggcgggcagatcacctggaggtcaggantttgagaccagcctggacc 362 63 agagagctaaattgccataggtacatttaaggcagtacacaggcatcagcactaaggcag 122 363 aacatggagaaaccccgtctctactaaaactacaaaattagtcaggcatagtggcgcacg 422 c-tgtaatcccagctactcaggaggctaaggcaggagaattgcttgaacctggggaaggc 481 gaatctctgatcctttatgatttcttctgcacattcttgtgagagggatttgggaaccca 62 Gaps 15-DEC-1995 est@watson.wustl.edu High quality sequence stops: 377 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL 183 ttgtcattagttagaatagcattgagcttgaagtgaaatgtaattagactgcgttatan School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University ; contact the IMAGE Consortium (info@image.llnl.gov) for further 8 Length 540; Indels <1..>540
BP; 153 A; 111 C; 135 G; 136 T; 5 other; N20091 473 bp mRNA EST yx36a12.s1 Homo sapiens cDNA clone 263806 3' 6 Score 468; DB 133; Pred. No. 0.00e+00; Mismatches /organism="Homo sapiens" Location/Qualifiers /clone="251941" information. NCBI qi: 1118383 /note="human' Query Match 30.0%; Best Local Similarity 96.8%; Matches 520; Conservative 473 g1124758 N20091 N20091 Sequence 540 9 source DEFINITION mRNA m 423 ACCESSION NID KEYWORDS RESULT SOURCE LOCUS 음 g g g 요 g, В g, გ В ی 용 g 유 g g a g

Aug 27 08:30 US-08-231-565A-1.rst

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vortebrata; Gnathostcomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archord; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
ONDRNAL Unpublished (1995)

JOURNAL Unpublished (1995)
OMMENT Contact: Wilson RK
WashU-Merck EST Project
WashIU-Merck Diversity School of Medicine

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 363
Source: IMAGE Consortium, LIMI
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MO 63108

4444 Forest Park Parkway, Box 8501, St. Louis,

4 151 /organism="Homo sapiens" Location/Qualifiers 6 97 /clone="263806" /note="human" 97 c <1..>473 NCBI gi: 1124758 1..473 127 source BASE COUNT FEATURES

Query Match 28.3%; Score 441; DB 112; Length 473;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 467; Conservative 0; Mismatches 2; Indels 4; Gaps

ORIGIN

4

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462 GCAAAAGTGTGAGAAATATTTCAGCATGTCTCAGGTGTCTCGCTGGCTCTTAAGGTG 403 241 qataaqqtqqtqqtqactqttctqqaqaqqtttctcataaqcaqqtqqqqqqaqaa 300	qu	121 9
402 AATAAGGTGGTGGTGTTCTCGAGAGTTTCTCATAAGGAGGTGAGATTGGGAA 343	දී :	522 (
301 ccacaggttcacagtttttctcttgaagagacactttgctgtcccgatgatcaaacctt 360 	d d	181 1 1 462 G
361 cttgtgggcatcttcttgttaagggcacattngagtgccaaccatggaagacttttatcc 420 	දි පී :	402 7
421 atcaaggetetgtatecatttegtettetacaataceaacageeggtgageag 473 	පු දු ද	301 0
SULT 10 HS091255 standard; RNA; EST; 473 BP. N20091;	දු දු	282 (421 8
17-DEC-1995 (Rel. 46, Created) 17-DEC-1995 (Rel. 46, Last updated, Version 1) yx36al2.sl Homo sapiens cDNA clone 263806 3′.	g	226 P
E.S.I. Homo sapiens (human) Enkaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.	RESULT LOCUS DEFINI ACCESS	RESULT 11 LOCUS DEFINITION ACCESSION
Hallier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hillier L., Clark N., Bubuque T., Le M., Lennon G., Marra M., Parsons J., Riffin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project"; "The WashU-Merck EST Project Washington University Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Parkway, Box 8501, St. Louis, Mo 63108 Feb. 314 206.1800 Feb. 314 206.18010 Feb.	NID KEYWORDS SOURCE	ORDS CE
extervation. This is the form of the constraint of the constraint, the clone is available royalty-free through LINI.  contact the IMAGE Consortium (info@image.llnl.gov) for further information. NCBI gi: 1124758  Location/Qualifiers	ORO	ORGANISM
source 1473 /organism="Homo sapiens" /clone="263806" /note="human" anRNA <1>473 Sequence 473 BP; 127 A; 97 G; 151 T; 1 other;	REFEI	REFERENCE AUTHORS
atch 28.3%; Score 441; DB 129; Length 473; sal Similarity 98.7%; Pred. No. 0.00e+00; 467; Conservative 0; Mismatches 2; Indels 4; Gap	TITLE JOURN COMMENT	TITLE JOURNAL MMENT
catgrattgcaacattattgatgagtttcccaatttatattttcccattcctc		

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Aug 27 08:30 US-08-231-565A-1 rst

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human clone=269080 primer=m13 -40 forward library=Soares melanocyte 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco 귭. RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. foreskin melanocytes (FS374) was kindly provided by Dr. Anthony cttgtgggcatcttcttgttaagggcacattngagtgccaaccatggaagacttttatcc 420 463 240 300 AATAAGGTGGTGGTGTCTTCTGCAGAGGTTTCTCATAAGCAGGTGGAGCATTGGGAA 343 360 283 227 1 (bases 1 to 433)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and 28-DEC-1995 ggcttgcattttcctacaccattccaaaggagaacattagatgtctgtattaaattcaa GGCTTGCATTTTTCCTACACCATTCCAAAGGAGAACATTAGATGTCTGTATTAAATTCAA gataaggtggtggtgactgtctgcagagagtttctcataagcaggtggagcattgggaa CTTGTGGGCCATCTTCTTGTTAAGG-CACATT-GAGTGCCAAC-ATG-AAGACTTTTATCC 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; yx91a09.s1 Homo sapiens cDNA clone 269080 3' Washington University School of Medicine Email: est@watson.wustl.edu The WashU-Merck EST Project Contact: Wilson RK WashU-Merck EST Project Unpublished (1995) Homo sapiens g1138827 Wilson, R Albino. N24677

Aug 27 08:30

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.

US-08-231-565A-1 mt

61 tcacatgattagtactgctagcggacctactaaaaattttaacactgacttattattagag 120 181 aagcaaaatgtgagagaaataatttcagcatgtctcaggtgtctcgctggctcttaagg 240 464 AAGCAAAAGTGTGAGAGAAATAATTTCAGCATGTCTCAGGTGTCTCGCTGGCTCTTAAGG 405 241 tgaataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattggg 300 584 TCACATGATTAGTACTGCTAGCGGACCTACTAAAATTTTAACACTGACTTATTATTAGAG 525 estëwatson.wustl.edu High quality sequence stops: 315 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; 301 aaccacaggttcacagtttttctcttgaagagacactttgctgtcccgattgatcaaacc 1 atcatncattgcaacatttattgatggagttttcccaatttaatatttctcatcatttcc 361 cctcttgtgggcatcttcttgttaaggcacattgagtgccaacatgaagacttttatcca School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University ; Query Match 27.1%; Score 423; DB 135; Length 433; Best Local Similarity 99.3%; Pred. No. 0.00e+00; Indels BP; 119 A; 85 C; 86 G; 142 T; 1 other; 2; 30-DEC-1995 (Rel. 46, Created) 30-DEC-1995 (Rel. 46, Last updated, Version 1) 0; Mismatches 絽 Location/Qualifiers HS796259 standard; RNA; EST; 396 N24796; /organism="Homo /clone="269080" "The WashU-Merck EST Project"; information. NCBI gi: 1138827 /note="human" 430; Conservative <1..>433 421 tcaaggctctgta 433 225 TCAAGGCTCTGTA 213 Sequence 433 Unpublished, source RESULT 13 Matches mRNA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARA 용 g g g, g ტ g გ 쇰 ģ 1 2 4 E 9 g 셤 გ 음 g Ξ 345 286 9 Gaps

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345 360 286 420 226

High quality sequence stops: 315 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the further information tgaataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattggg 300 atggcttgcattttcctacaccattccaaaggagaacattagatgtctgtattaaattc 180 aagcaaaagtgtgagaaataatttcagcatgtctcaggtgtctcgctggctcttaagg 240 aaccacaggttcacagtttttctcttgaagagacactttgctgtccgattgatcaaacc 360 cctcttgtgggcatcttcttgttaaggcacattgagtgccaacatgaagacttttatcca 420 644 ATCATGCATTGCAACATTTATTGATGGAGTTTTCCCAATTTAATATTTCTCATCATTTCC 585 tcacatgattagtactgctagcggacctactaaaaattttaacactgacttattattagag 120 285 CTTCTTGTGGGCATCTTCTTGTTAAGGCACATTGAGTGCCAACATGAAGACTTTTATCCA 226 1 atcaincaitgcaacatttattgatggagttttcccaatttaatatttctcatcatttcc 404 TGAATAAGGTGGTGGTGACTGTTCTGCAGAGTTTCTCATAAGCAGGTGGAGCATTGGG AACCACAGGTTCACAGTTTTTCTCTTGAAGAGACACTTTGCTGTCCCGAT-GATCAAACC ij Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Length 433; 1 others Indels (info@image.llnl.gov) for Score 423; DB 113; Pred. No. 0.00e+00; 0; Mismatches 2; 30-DEC-1995 (Rel. 46, Created) 30-DEC-1995 (Rel. 46, Last updated, Version 1) yx91a09.s1 Homo sapiens CDNA clone 269080 3'. 142 /organism="Homo sapiens" /clone="269080" /note="human" sequence stops: 315 Location/Qualifiers ð HS677260 standard; RNA; EST; 433 98 27.1%; 99.3%; 85 c 430; Conservative <1..>433 IMAGE Consortium NCBI gi: 1138827 1..433 TCAAGGCTCTGTA 213 tcaaggctctgta 433 Homo sapiens (human) Best Local Similarity 119 Query Match N24677; source BASE COUNT 1 - 433225 61 121 181 241 301 344 361 421 Matches FEATURES RESULT
1D HS
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RESULT LOCUS

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Gaps

Indels 0;

Length 396;

2 others

human clone=269707 primer=m13 -40 forward library=Soares melanocyte 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; This clone is available royalty-free through LLNL ; contact the MAGE Consortium (info@image.linl.gov) for further information. 644 ATCATGCATTGCAACATTTATTGATGGAGTTTTCCCAATTTAATATTTCTCATCATTTCC 585 1 atcatncattgcaacatttattgatggagttttcccaatttaatatttctcatcatttcc 60 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

 (bases 1 to 396) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; yx97f10.s1 Homo sapiens cDNA clone 269707 3' ; Score 394; DB 113; Pred. No. 0.00e+00; 0; Mismatches ¥ 131 /organism="Homo sapiens" High quality sequence stops: 310 Source: IMAGE Consortium, LLNL Location/Qualifiers ð Email: est@watson.wustl.edu The WashU-Merck EST Project 8 Contact: Wilson RK WashU-Merck EST Project /clone="269707 /note="human" Query Match 25.3%; Best Local Similarity 99.7%; 75 c Matches 394; Conservative Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 <1..>396 NCBI qi: 1138946 Homo sapiens Wilson, R. q1138946 108 Albino. DEFINITION source ORGANISM BASE COUNT JOURNAL ACCESSION REFERENCE AUTHORS KEYWORDS FEATURES TITLE SOURCE COMMENT ORIGIN 쇰 g 염 g 쇰 ö aagcaaaagtgtgagagaaataatttcagcatgtctcaggtgtctcgctggctcttaagg 240 tcacatgattagtactgctagcggacctactaaaaattttaacactgacttattattagag 120 atggettgeatttteetacaccatteeaaaggagaacattagatgtetgtattaaatte 180 524 AIGGCIIGCAITITICCIACACCAIICCAAAGGAGAACAIIAGAIGICIGIAIIAAAIIC 465 AAGCAAAAGTGTGAGAAAAAAATTTCAGCATGTCTCAGGTGTCTCGCTGGCTCTTAAGG 405 tgaataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattggg 300 TGAATAAGGTGGTGGTGATGTTCTGCAGAGATTTCTCATAAGCAGGTGGAGCATTGGG 345 aaccacaggttcacagtttttctcttgaagagacactttgctgtcccgatgatcaaaccc 360 1 atcatncattgcaacatttattgatggagttttcccaatttaatatttctcatcatttcc 60 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsone J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project"; est@watson.wustl.edu High quality sequence stops: 310 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: contact the IMAGE Consortium (info@image.llnl.gov) for further ö Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Length 396; Indels Sequence 396 BP; 108 A; 75 C; 80 G; 131 T; 2 other; EST Score 394; DB 136; Pred. No. 0.00e+00; yx97f10.sl Homo sapiens cDNA clone 269707 3' TTCTTGTGGGCATCTTCTTGTTAAGGCACATTGAG 250 ttcttgtgggcatcttcttgttaaggcacattgag 395 0; Mismatches /organism="Homo sapiens" mRNA Location/Qualifiers /clone="269707" information. NCBI gi: 1138946 /note="human" ል Query Match 25.3%; Best Local Similarity 99.7%; 394; Conservative 396 <1..>396 Homo sapiens (human)

Matches

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Job time : 642 secs

NCBI gi: 1140910

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Source: IMAGE Consortium, LLNL

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ö 240 464 AAGCAAAAGTGTGAGAGAAATATTTCAGCATGTCTCAGGTGTCTCGCTGGCTCTTAAGG 405 241 tgaataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattggg 300 345 aaccacaggttcacagtttttctcttgaagagacactttgctgtcccgatgatcaaaccc 360 61 tcacatgattagtactgctagcggacctactaaaaattttaacactgacttattattagag 120 8 Gaps 181 aagcaaaagtgtgagagaaataatttcagcatgtctcaggtgtctcgctggcncttaagg 344 AACCACAGGTTCACAGTTTTTCTCTTGAAGAGACACTTTGCTGTCCCGATGATCAAACCC 1 atcatgcattgcaacatttattgatggagttttcccaatttaatatttctcatcatttcc ö Length 401 1 others Indels Score 392; DB 114; Pred. No. 0.00e+00; 0; Mismatches 284 TTCTTGTGGGCATCTTCTTGTTAAGGCACATTGAG 250 ų 129 ttcttgtgggcatcttcctgttaaggcacattgag /organism="Homo sapiens' Search completed: Tue Aug 27 08:43:15 1996 Location/Qualifiers δ 82 /clone="266361" /note="human" Query Match 25.1%; Best Local Similarity 99.5%; Matches 393; Conservative 79 c <1..>401 1..401source BASE COUNT 361 301 FEATURES ORIGIN 용 g გ g 쇰 გ g 음 임 გ 음 გ 음 g

SUMMARIES

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm MPsrch\_nn

n.a.

MasPar time 1034.82 Seconds 1145.061 Million cell updates/sec Tue Aug 27 08:07:40 1996; Run on:

not generated. Tabular output

(1-1559) from US08231565A.seq >US-08-231-565A-1 Title:

1559 Description: Perfect Score:

N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch 270440 seqs, 380027776 bases x 2 Searched:

Minimum Match 0% Post-processing:

Listing first 45 summaries

embl-new3 Database:

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLIN 9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:URT

16:VIR1 17:VIR2

genbank 92 Database:

9-EIGHT 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5 32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PBC 39:PLM1 40:PLM2 41:PLM3 42:PLM3 43:PLM5 44:PLM5 47:PM1 48:PM12 49:PLM3 64:PLM5 44:PLM5 47:PM1 48:PM12 49:PM13 50:PM14 51:PM15 52:PM16 53:PM17 54:PM18 55:PM19 65:PM10 57:PM110 58:PM10 59:PM11 60:ROD1 61:ROD2 62:ROD3 63:ROD3 64:ROD5 65:ROD5 65:ROD5 65:ROD5 67:PM1 71:VML2 72:VML3 73:VML4 74:VML5 75:VML6 76:VML7 77:VMT1 78:VMT2 79:VMT3

80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PIN 86:PRI 87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT u-emb145 92 genbank-new1

Database:

93:part1 Database:

Mean 12.154; Variance 9.393; scale 1.294 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Homo sapiens Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Human melanoma antigen recognized by T-cells (MART-1) mRNA. U06452

1524 bp

g476131 human.

DEFINITION ACCESSION

RESULT rocus KEYWORDS SOURCE ORGANISM

ALI GNMENTS

		Kot V	Match Longth	DB	QI	Description	Pred. No.
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	1 1524	97.8	1	i	HSU06452	Human melanoma antige	0.00e+00
	2 645			52	HSU06654	Human differentiation	0.00e+00
v	7	15.3	291		HSU14572	***ALU WARNING: Human	2.14e - 104
		15.3	35962		HSBLGR1	Human ABL gene, exon	7.33e-104
	7	15.3	35962	-	HSABLGR1	Human ABL gene, exon	7.33e-104
	6 238	15.3	35962		HSABLGR1	Human ABL gene, exon	7.33e-104
ບ	7 237	15.2		-	HSATPCP1	for	2.51e-103
	8 232	14.9	6901		HSLCATG	H. sapiens gene for le	1.19e-100
· U		14.9			HSTMP04		1.19e-100
-		14.9	_		HSPROSCHY	H. sapiens genes for p	1.19e-100
c 1		14.9	16851		HSL69F7B	Human DNA sequence fr	1.19e-100
-	2 233		7		HSF LNG6PD		3.46e - 101
		14.9		10	HSFLNG6PD	Homo sapiens chromoso	1.19e-100
_					HUMTGTPV2		1.39e - 99
_		14.8			HSL174G8C	Human DNA sequence fr	1.39e - 99
_			m		HSL139H8	Human DNA sequence fr	4.06e-100
, <sub>U</sub>	7 229				HSU14573	***ALU WARNING: Human	4.75e-99
		14.7	36594		HUMTPA	Human tissue plasmino	4.75e-99
		14.6	m		HUMRCC1	Human RCC1 gene, comp	5.56e-98
7		14.5			HSL174G8B	Human DNA sequence fr	1.90e-97
c 5		•			HSUBA52G	UPA52	
~		•			HUMATPSAS		1.90e-97
ر 2		•			HUMLHDC	gene	
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CV3		•		4	HSABLGR3		1.90e-9/
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7		14.5			HSABLGR3	o-oncoden	•
	28 225	14.4			HSRJ14	sequence	6.49e - 97
		14.4			HSL95E6	sequence	2.22e-96
ຕ		14.4			HSL95E6	Human DNA sequence fr	2.22e-96
m		14.4	37785		HUMXRCC1G		2.22e-96
ຕ	32 224	14.4			HUMDXS455A	···	. 22e-
(1)		14.4	4		HSU141H12		.49e-
c o		14.2			HUMIL11A	Human interleukin 11	8.83e-95
m		14.2			HSMOGG	dene	.59e-
m	36 222	14.2	_		HSMOGG	gene for	.59e-
m		14.2	7		HSL165D7	sequence	.59e-
m	38 222	14.2			HSL165D7	Human DNA sequence fr	.59e-
(1)	39 221	.14.2			HSL30G1	Human DNA sequence fr	.83e-
4	0 222	14.2	40592		HSL191F1	Human DNA sequence fr	
7	_	14.2		~	HSL191F1	Human DNA sequence fr	.59e-
Þ	2 222	14.2		23	HSU24498	Human autosomal domin	.59e-
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Eutheria;	qq	421 gacacctgagacatgctgaaattattctctc
REFERENCE 1 (bases I to 1524) AUTHORS Kawakami,Y., Elismon,S., Delgado,C.H., Robbins,P.F., Rivol	voltini, L., Qy	421
IOPALIAN, D.L., PLAL, I. and ROSENDELY, J. A.  TITLE Cloning of the gene coding for a shared human melanoma antigen recomnized by autologous T cells infiltrating into tumor	antigen Db r	481 tctaatgttctcctttggaatggtgtaggaaa
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91, 3515-3519 (1994) MEDLINE 94224770	δλ	481
	qa	541 gtgttaaaattttagtaggtccgctagcagta
Agrandant, Nimert Submission Submitted (08-PFR-1994) Vutaka Kawakami, Surgery	Qy . National	541
Cancer Institute, National Institutes of Health,	9000 Rockville Db	601 attaaattgggaaaactccatcaataaatgtt
	Qγ	601
FEATURES Location/Qualitiers source 11524	qa · · · · · · · · · · · · · · · · · · ·	661 gtaatgttagtaaatccatggtgttattttct
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/gene="MART-1"	•	
/standard_name="melanoma antigen recognized by T- /note="NCBI qi: 476132"	T-cells" UY	17/
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/db_xret="Y.D.;d4\615.2 /translation="MPREDAHFIYGYPKKGHCHSYTAEEAAGIGILTVILGVLLLIG	LTVILGVLLLIG	781
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BASE COUNT 435 a 330 c 324 g 435 t ORIGIN	δδ	841
Query Match 97.8%; Score 1524; DB 52; Length 1524;	qa	901 agcaatgtctctttgtgctctaaaattctatt
Vred. No. 0.00e+00; 0; Mismatches 0; Indels 0;	Gaps 0; Qy	901
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Qy 1 AGCAGACACAGAGACTCTCATTAAGGAAGGTGTCCTGTGCCCTGACAAGATGCCAA	CAA 60 Qy	961
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Qy 61 GAGAAGATGCTCACTTCATCTATGGTTACCCCAAGAGGGGCACGGCCACTCTTACACCA	cca 120 Qy	1021
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Qy 121 CGCTGAAGAGGCCGCTGGGATCGCATCTGACAGTGATCTGGGAGTCTTACTGCTCA	TCA 180 Qy	1081
Db 181 tcgctgttggtattgtagaagacgaaatggatacagagccttgatggataaaagtcttc	ttc 240 Db	o 1141 gtagagacggggtttctccatgttggtcaggc
Qy 181 TCGCTGTTGGTATTGTAGAAGACGAAATGGATACAGAGCCTTGATGGATAAAAGTCTTC	TTC 240 Qy	1141
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٥y	601	TTAATTIGGGAAAACTCCATCAATAAATGTTGCAATGCATGATACTATCTGTGCGGAGA	
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Ωy	721	CTCTTTACTTGAAATTTGGCTAATAACAAACTAGTCAGGTTT	
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φ	781	CACAGAATTGTTCCAGTACTATGGAGTGCTCACAAAG	
Op	841	tacttttacaggttaagacaaagggttgactggcctatttatctgatcaagaacat	
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ð	1021		
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ΩP	1141	gagacggggtttctccatgttggtcaggctggtctcaaactcctga	
δλ	1141	CATGITGETCAGGCTGGTCTCAAACTCCTGACCTCAGGTG	
qq	1201	ctgccgcctcagcctcccaaagtgctggaattacaggcgtgagccaccacgcctggctg 1260	
οy	1201	TECCCECCTCAGCCTCCCAAGTGCTGGAATTACAGGCGTGAGCCACCACGCCTGGCT	
Dp	1261	gatcctatatcttaggtaagacatataacgcagtctaattacatttcacttcaaggctca 1320	
δý	1261	rcctatatcttaggtaagacatataacgcagtctaattacattcacttcaaggctc	
QQ	1321	ctactaaaccagaaattggtagaaggattta 138	
δλ	1321	SCTATTCTAACTAATGACAAGTATTTTCTACTAAACCAGAAATTGGTAGAAGGATTT	

g δ g ð Бb δ

aatcataaaggatcagagattctg 1524 

1501

1441 acctatggcaatttagctctcttgggttcccaaatccctctcacaagaatgtgcagaaga

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ö teggetgttggtattgtagaagaegaaatggatacagageettgatggataaaagtette 347 atgitggcactcaatgigccttaacaagaagatgcccacaagaagggttigatcaicggg 407 227 287 TCGGCTGTTGGTATTGTAGAAGACGAAATGGATACAGAGCCTTGATGGATAAAAGTCTTC 240 acagcaaagtgtctcttcaagagaaaaactgtgaacctgtggttcccaatgctccacctg 467 agcagacagaggactctcattaaggaaggtgtcctgtgccctgaccctacaagatgccaa 167 1 AGCAGACAGAGGACTCTCATTAAGGAAGTGTCCTGTGCCCTGACCCTACAAGATGCCAA 60 Gaps cggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtcttactgctca gagaagatgctcacttcatctatggttaccccaagaaggggcacggccactcttacacca ; 0 Length 752; 0; Indels Score 645; DB 52; Pred. No. 0.00e+00; 0; Mismatches Query Match 41.4%; Best Local Similarity 100.0%; 645; Conservative 241 Matches 108 168 61 228 121 288 181 348 408 셤 В 8 ð ò 염 ð

468 셤

CTTATGAGAAACTCTCTGCAGAACAGTCACCACCACCTTATTCACCTTAAGAGCCAGCGA 420 361 δ

tctaatgttctcctttggaatggtgtaggaaaatgcaagccatctctaataataagtca 647 421 588 à g

gtgttaaaattttagtaggtccgctagcagtactaatcatgtgaggaaatgatgagaaat 648 qq

ð

601 à

17-NOV-1994 HSUI4572 291 bp DNA SYN 17-NOV-1 \*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence. U14572 9551541 human. SOURCE ORGANISM DEFINITION NID KEYWORDS ACCESSION

Eukaryotae; Hyperchondria; Eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Choanata;

180

б

163

170 c

æ

239

BASE COUNT

/note="8 A residues"

730..735 752

polyA\_signal polyA\_site

exon

ORIGIN

S

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Homo sapiens

ORGANISM

REFERENCE AUTHORS

human.

Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 752)

Coulie, P.G., Brichard, V., Van Pel, A., Wolfel, T., Schneider, J., Traversari, C., Mattei, S., De Plaen, E., Lurquin, C., Szikora, J.P., Renauld, J. and Boon, T.

new gene coding for a differentiation antigen recognized by autologous cytolytic T lymphocytes on HLA-A2 melanomas (see

J. Exp. Med. 180, 35-42 (1994) 94275389

JOURNAL MEDLINE

REFERENCE AUTHORS

comments]

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TITLE

(bases 1 to 752)

Coulie, P.

TITLE JOURNAL

Human differentiation antigen melan-A protein mRNA, complete cds. U06654 9517022

7

RESULT

DEFINITION

ACCESSION NID

KEYWORDS

301 δ

cttatgagaaactetetgeagaacagteaceaceaecttatteaecttaagageeagega 527

528

Direct Submission Submitted (11-FEB-1994) Pierre Coulie, Ludwig Institute for Cancer Research, Brussels Branch, Avenue Hippocrate 74, UCL 7459,

/organism="Homo sapiens" 1..135

Location/Qualifiers

...752

source

FEATURES

COMMENT

exon

B-1200, Belgium

Brussels,

NCBI gi: 517022

481

δ

707

541

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335..448 449..752

/note="NCBI gi: 517023"

/number=2 /number=1

136..237 161..517

exon

CDS

/codon\_start=1

Submitted (09-SEP-1994) Wojciech Makalowski, National Center for Biotechnology Information, NIH, 8600 Rockville Pike, Bethesda, MD interspersed within the human genome with an average spacing of 4 kb. Some Alus are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' sequence in any orientation. Although Alu elements (especially be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions. With the consemence CAUTION: This consensus Alu entry is provided to help identify Alu-derived sequences in newly determined nucleotide sequences been overlooked on several occasions, with the consequence erroneous Alu-derived amino acid sequences being reported. to create additional/alternative exons, consideration should situated on the complementary strand) have a great potential untranslated regions. However, cDNA libraries also contain partial and/or rearranged cDNAs ligated with an Alu-derived CAUTION: Alu repetitive elements, unique to primates, are CAUTION: Any significant similarity of a putative protein Jurka, J. and Milosavljevic, A. Reconstruction and analysis of human Alu genes J. Mol. Evol. 32 (2), 105-121 (1991) 91178815 Claverie, J-M. and Makalowski, W. Makalowski, W. and Claverie, J-M. Nature 371, 752-752 (1994) (bases 1 to 291) (bases 1 to 291) (bases 1 to 291) Direct Submission Alu alert 95021758 REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL REFERENCE AUTHORS MEDLINE MEDLINE REFERENCE AUTHORS COMMENT

possibility of false negative results may also occur when searching in the coding nucleotide sequence. Furthermore, the possibility a putative protein sequence against these consensus sequences. identified by a match against these consensus sequences. The sequence with this entry must be taken as a warning that a portion of an Alu repeat may have been artificially included exists that the full extent of an Alu sequence may not be

CAUTION: Discovery of Alu-like sequence(s) in DNA of non-primate origin should be considered as a warning that contamination has

have been constituted and added to GenBank; accession numbers U14567, U14568, U14569, U14570, U14571, U14572, U14573 and U14574 Various analyses (see reference 2) indicate that Alu repeats fall 8 ALU WARNING consensus sequences into 8 subfamilies. Therefore,

Location/Qualifiers NCBI gi: 551541 source FEATURES

/organism="Homo sapiens" /citation=[2]

45 t 94 g 80 c æ 72 BASE COUNT ORIGIN

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1258 GCCAGGCGTGGTGGCTCACGCCTGTAATTCCAGCATTTGGCAGGCTGAGGCGGGCAGAT 1199 පු გ

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aaaatacaaaaattagccgggcgtggtggcgcatgcctgtaatcccagctactcgggagg 181 122 임 g

ctgaggcaggagaatcgcttgaacccgggaggcggaggttgcggtgagccgagatcgcgc 241 182 გ 임

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Bb standard; DNA; PRI; 35962 HSBLGR1 U07561; RESULT

23-JUL-1994 (Rel. 40, Created) 31-JAN-1996 (Rel. 46, Last updated, Version 15)

Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.

Homo sapiens (human)

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

1 - 35962

Chissoe S.L., Bodenteich A., Wang Y., Jian L., Burian D., Carbtree J.S., Freeman A., Hamed O.S., McLaury H., Pan H., Toth S., Wang Z., Zhang G., Clifton S., Groffen J.,

Sequence and analysis of the human ABL gene, the BCR gene, and Heisterkamp N., Roe B.A.;

regions involved in the Philadelphia chromosomal translocation";

MEDLINE; 82199444.

Genomics 27:67-82(1995).

Groffen J., Heisterkamp N., Grosveld F., de Ven W.,

Stephenson J.R.;

"Isolation of human oncogene sequences (v-fes homolog) from cosmid library"; Science 216:1136-1138(1982)

MEDLINE; 91329820.

Morris C.M., Heisterkamp N., Groffen J., Fitzgerald P.H.; "Entire ABL gene is joined with 5'-BCR in some patients with Philadelphia-positive leukemia"; Blood 78:1078-1084(1991).

27793-28338, 28792-29265

gene Shtivelman E., Lifshitz B., Gale R.P., Roe B.A., Canaani E.; "Alternative splicing of RNAs transcribed from the human abl and from the bcr-abl fused gene"; MEDLINE; 87028219. 

Cell 47:277-284 (1986).

27108-29899

MEDLINE; 88038877.

US-08-231-565A-1.rge Aug 27 08:17

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E I	repeat_region	(1907.1915) 2184
<b>:</b>		/citation=[10] /rnf familv="Alu"
ᇤ	repeat region	21852227
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H		/rpt_family="Alu"
. i	repeat_region	34343174
r fr		/rot family="Alu"
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FT	l	/citation=[10]
<u>.</u>	1	4
1 5	repeat_region	complement((3/98.3804)6146/ /citation=[10]
Ë		/rpt family="Alu"
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→ E→	repeat region	/rpc_tanily= Aid 65106820
FT	-	/citation=[10]
E E	40000	/rpt_family="Alu" //6000_6000\ /7280_7240\
F. E.	Tebear Teaton	Comprement (10500,0550)(7205,755)/ /citation=[10]
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댐.		/note="putative 8604 MET gene, 5' to the ABL gene; NCBI gi
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>		
F.		ILGNNGFIWIYPTPEHKEEEAGGFIANLEPVSLADREVISRLRNCIISLVTQRMMLYD
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KEYWORDS ö Db 15175 tttttttgagacggagtttcactcttgttgcccaggctggagtgcaatggtgggatctcg 15234 971 TTTTTTGAAGGAGTTTCGCTTTTGTTGCTCCCAGGCTGGAGTGCAATGCCGCGATCTT 1030 Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.

9514262 Gaps 0; Mismatches 25; Indels 0; Score 238; DB 9; Length 35962; Pred. No. 7.33e-104; Db 15415 cagoctoccaaatgctgggattacaggtgtgagccaccgcacctggc 15462 Qy 1211 CAGCCTCCCAAAGTGCTGGAATTACAGGCGTGAGCCACCACGCCTGGC 1258 /rpt\_family="Alu" complement((14984.15063)..(15359.15379)) /rpt\_family="Alu" complement((13422.13425)..13719) /rpt\_family="Alu" complement((15133.15140)..15489) /citation=[10] /product="unknown"
(14674.14676)..(15029.15040) /rpt\_family="Alu" complement(13922..14172) /citation=[10] /rpt\_family="Alu" 14134..14199 /rpt\_family="Alu" complement(10906..10991) /citation=[10] complement (12599..12899) /rpt\_family="Alu" 13035..(13382.13389) /product="unknown" /rpt\_family="Alu" 12388..12433 Note: remainder of annotations omitted. /citation=[10] /citation=[10] citation=[10] /citation=[10] /citation=[10] Query Match 15.3%; Best Local Similarity 91.3%; Matches 263; Conservative /number=3 /number=4 repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region S DEFINITION ACCESSION NID exon exon RESULT Бb ð 염 δ 담담담 ð

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REFERENCE 10 (sites)			OUGNAL UNDULLEGA		Bartram, C.R. and Grosveld, G.	TITLE Philadelphia chromosomal breakpoints are clustered within a limited	JOURNAL Cell 36 (1), 93-99 (1984)			S	1111L Sequence Of the number and and of peres Indianal, Thesis (1904) Injuracity of Oklahom			Direct Submission	JOURNAL Submitted (08-MAR-1994) Bruce A. Roe, Dept. of Chem. and Blochem.,	University of Oklahoma, 620 Parrington Oval, Km 208, Norman, Ok	COMMENT NCRI of: 514262	S	rce	/ CDTGOOGGE-V.	/map= 7404 /ordanism="Nomo sapiens"	/tissue type="lung carcinoma"	/citation=[2]	/citation=[3]	/citation=[12] renest region complement(448783)			repeat_region_complement(4/8(/26./28)}	/ipc_idmin_ Aid /citation=[10]	repeat_region 1012(1327.1338)	/rpt_tamily="Aiv" /citation=[10]	repeat_region complement(14551786)	/rpt_family="Alu" /cit=fin=1101	repeat region (1907.1915)2184	/rpt_family="Alu"	/citation=[10] rangst radion		repeat_region complement(26192894) /rot_familv="Alu"		repeat_region 34543774		repeat_region (4049.4097)(4411.4433)	/rpc_raming_/rich /citation=[10]	repeat_region complement((5798.5804)6146)		repeat_region complement(6412(6677.6691))

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Philadelphia chromosomal breakpoints are clustered within a limited
                                                                                                                                                                                                     The first intron in the human c-abl gene is at least 200 kilobases long and is a target for translocations in chronic myelogenous \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-MAR-1994) Bruce A. Roe, Dept. of Chem. and Biochem., University of Oklahoma, 620 Parrington Oval, Rm 208, Norman, OK
                                    Shtivelman, E., Lifshitz, B., Gale, R.P., Roe, B.A. and Canaani, E. Alternative splicing of RNAs transcribed from the human abl gene and from the bcr-abl fused gene
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Bartram, C.R. and Grosveld, G.
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Characterization of the human ABL promoter regions
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                 (bases 27793 to 28338; 28792 to 29265)
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A catalogue of splice junction sequences
Nucleic Acids Res. 10 (2), 459-472 (1982)
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Human ABL gene, exon 1b and intron 1b, and putative M8604 Met
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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	RESULT 7 LOCUS HSATPCP1 9457 bp DNA PRI 19-JUL-1993 DEFINITION H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form). ACCESSION X69907 NID 938429 KEYWORDS ATP synthase; ATP synthase c subunit. SOURCE human. ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;	Metazoa; Eumetazoa; Bilateria; Cocomata; Deuterostomia; Chordata; Metazoa; Eumetazoa; Bilateria; Cocomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Vertapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 9457) AUTHORS Walker, J.E.  TITLE Direct Submission JOURNAL Submitted (29-DEC-1992) to the EWBL/GenBank/DDBJ databases. J.E. Halker, M.R.C. Lab. of Molecular Biology, Hills Road, Cambridge CB2 20H. UK	E 2 (bases S Dyer, M.R. Sequences mitochond L Biochem. E 9319529	FEATURES Location/Qualifiers source 19457 /organism="Homo sapiens" /cell_type="T-cell" /cell_line="AT5B1" /clone_lib="lambda 2001"	repeat_unit 1224  repeat_unit 273442  repeat_unit 606904  repeat_unit 606904	it it it it	GC signal 4001.4046  repeat unit 4000.44792  /rpt family="Alu"  CAAT signal 4538.4542  CAAT signal 4641.4645  CAAT signal 4671.4701  TATA signal 4671.4701  TATA signal 4081.4713  mRNA 1961.4713  mRNA 1961.4713  mRNA 1961.4713  prim_transcript 4733.7802  /gene="Pl gene for c subunit of human mitochondrial ATP synthase"  /gene="Pl gene for c subunit of human mitochondrial ATP synthase" /gene="Pl gene for c subunit of human mitochondrial ATP // 1733.7802

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Gaps

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PRI

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6905 bp

HSTMP04

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RESULT LOCUS

8998 aaaaatacaaagttaaccaggcatggtggcgatgctgtaatcccagctacttgggagg 9057	HSLCATC 6901 bp DNA PRI 24-APR-1993 H.sapiens gene for lecithin-cholesterol acyltransferase (LCAT). X04981 434286 Alu repetitive sequence; phosphatidylcholine-sterol acyltransferase; signal peptide. Alu repetitive sequence; phosphatidylcholine-sterol acyltransferase; signal peptide. Homo sapiens Enkaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarchini; Hominidae; Homo. I (bases I to 6901) McLean, J., Wion, K., Drayna, D., Fielding, C. and Lawn, R. Human lecithin-cholesterol acyltransferase gene: complete gene sequence and sites of expression Nucleic Acids Res. 14 (23), 9397-9406 (1986) See M12625 for LCAT mRNA Data kindly reviewed (14-JUL-1987) by McLean J.	Incation/Qualifiers  Location/Qualifiers  16901  /organism="Homo sapiens" /close lib="(lambda)charon30"  /gnal
8998 aaa      1139 AAA  0058 ctg     1079 CTA      11019 CAT	SINTION SINTION SINTION ORDS CCE CGANISM CGANISM CTILE DURNAL DUINE CENT	NCBI qi: source CAAT_signal TATA_signal Prim_transcript exon CDS intron
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join(U18266:2201..2479,U18267:120..246,U18268:130..288,
39..1558)
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LPCTSNSMPPLDVENIQKRIDQSKFQETEFLSPPRKVPRLSEKSYEERDSGSFVAFQN
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for
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Submitted (07-DEC-1994) Crafford A. Harris, Immunobiology Research
Institute, Route 22 East, Annandale, NJ 08801-0999, USA
                                                                                                                                                                                                      Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Human thymopoietin (TMPO) gene, exons 4 and 5, and complete cds
                                                                                                                                                                                                                                                                                                                                                                   Structure and mapping of the human thymopoietin (TMPO) gene and relationship of TMPO beta with rat lamin-associated polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Placenta genomic library in lambda FIX II;
                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
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Larsen, F., Solheim, J., Kristensen, T., Kolsto, A.B. and Prydz, H. A tight cluster of five unrelated human genes on chromosome 16q22.1 Hum. Mol. Genet. 2 (10), 1589-1595 (1993) Eukaryočae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Terrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. ö Submitted (10-MAY-1993) to the EMBL/GenBank/DDBJ databases. F. Larsen, Biotechnology Centre of Oslo, University of Oslo, PO Box 1125 Blindern, N0317 Oslo, NORWAY 1258 GCCAGGCGTGGTGGCTCACGCCTGTAATTCCAGCACTTTGGGAGGCTGAGGCGGCAGAT 1199 CpG island; gene cluster; proteasome subunit; serine protease; serine protein kinase. 11-NOV-1993 chymotrypsin-like protease (CTRL-1) and protein serine kinase Gaps aaaatacaaaattagccaggcatggtggtgcatgcctgtaatcctagctactccggaggc ö H.sapiens genes for proteasome-like subunit (MECL-1), . 6412 attgcactctagcctgggcaacaagagcgaaactctgtctcaaaaataaa 6461 Indels PRI Pred. No. 1.19e-100; 0; Mismatches /clone\_lib="cosmid c0S202" /clone="cos0DIN" /organism="Homo sapiens" /cell\_type="leukocytes" 123..423 513..805 /note="Alu repeat" 566..571 Location/Qualifiers 1..13863 DNA /note="Alu repeat" /map="16q22.1 13863 bp Best Local Similarity 90.0%; 261; Conservative (PSK-H1) last exon. Direct Submission 406226 Homo sapiens HSPROSCHY NCBI gi: Larsen, F. g406226 X71874 human. repeat\_unit repeat unit 10 DEFINITION source ORGANISM Matches 6292 TITLE JOURNAL AUTHORS AUTHORS JOURNAL MEDLINE

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ora Sim	misc_feature	/note="signal peptide" /number=2 78957939 /note="activation peptide"
mis mat int	misc_feature mat_peptide intron	79407996 /label=stl join(79407996,80958174,82878368,85068686, 87748907,89989159) /product="chymotrypsin-like protease CTRL-1"
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complement (join (<1187..1313, 7404..7606, 8663..8815, 10383..
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1316..1353
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Note: remainder of annotations omitted.
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8998..9210
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8998..9484
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Best Local Similarity 88.9%;
                                                                                   8998..9159
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Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, This sequence is not the entire insert of clone L69F7B. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems such as compressions and repeats, but not necessarily within known The sequence from clone L161A8 has been finished in more than one The library was constructed using flow-sorted human chromosome 4 from a Hamster-Human hybrid cell line ( UV20HL21-27 ) containing sequence is ambiguous, there is an annotation using the "unsure" See also Myers et al, Cytogenet Cell Genet. 66 (1994) Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Human Genome Center, Los Alamos National Laboratory, NM 87545 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; This sequence (1161A8B) is separated from the preceeding one (1161A8A) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail Submitted (16-FEB-1996) to the EMBL/GenBank/DDBJ databases L69F7 is contained in a clone contig spanning -2Mb which described in Baxendale et al, Nature Genetics 4 ( 1993 ) L69F7 is from cosmid library LA04NC01 constructed at the chromosome 4p16.3 contains Huntington Disease (HD) gene. annotated human repeat sequence elements (e.g. Alu). US-08-231-565A-1 rge under the auspices of the U.S. Department of Energy 22-FEB-1996 (Rel. 46, Last updated, Version 1) true left end of clone L161A8 is at 16748. /clone\_lib="LA04NC01" /cell\_line="UV20HL21-27" sapiens" 4p16.3; Huntington Disease (HD) gene. Location/Qualifiers organism="Homo human fchromosomes 4, 8 and 21. enquires: humquery@sanger.ac.uk /clone="L69F7B" chromosome="4" 22-FEB-1996 (Rel. 46, Created) /map="4p16.3" Aug 27 08:17

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ö Db 11704 gccaggcatggtggctcacacctgtaatcccagcactttgggggggtcgaggaggcggat 11763 11824 aaaatacaaaattagccgggcatggtggtgcatgcctgtaatcccagctactcaggaggc 11883 11884 tgaggcaggagaattgcttgaacccgggaggtggaggttgtggtggtgagctgagatcatgcc 11943 1258 GCCAGGCGTGGTGGCTCACGCCTGTAATTCCACCACTTTGGGAGGCTCAGGCGGGCAGAT 1199 Gaps Department of Molecular Microbiology and Center for Genetics in Medicine Washington University School of Medicine, St. Louis MO 63110 USA email: ellson@genseq.apldbio.com and davids@genetics.wustl.edu Note: Gene predictions were accomplished with runs of Grail Versions 1.1 and 1.2, coupled with fasta and blastx comparisons to genbank & non-redundant peptide libraries. Submitted by: Ellson Chen, Advanced Center for Genetic Technology, Applied Biosystems Division of Perlin Elmer Corp., 850 Lincoln Center Drive, Foster City, CA 94404 USA and David Schlessinger, G6PD gene; gdi gene; GdX gene; glucose-6-phosphate dehydrogenase; P3 gene; QM gene; STA gene; XAP-1 gene; XAP-2 gene; XAP-4 gene; XAP-5 gene; XAP-7 gene. "Thirteen known and six candidate genes in 219.4kb of high GC DNA between the human RCP/GCP and G6PD loci"; emery-dreyfuss syndrome; filamin; FLN gene; G4.5 gene; G4.8 gene; Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.N., Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D., D'Urso M.; /partial 1682..1966 /note="Alu repeat: matches 308..1 of consensus" Score 232; DB 10; Length 16851; Pred. No. 1.19e-100; 0; Mismatches 29; Indels 0; glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Db 11944 attgcactccagcctgggcaacaagagcaaaactctgtctcaaaaaaa 11993 Sequence 16851 BP; 5048 A; 3835 C; 3519 G; 4449 T; 0 other; Homo sapiens chromosome X region from filamin (FLN) gene to 1A gene; 2\_19 gene; ABP-280 gene; actin-binding protein; DNase I-like protein gene; DNL1L gene; EMD gene; emerin; 29-FEB-1996 (Rel. 47, Created) 29-FEB-1996 (Rel. 47, Last updated, Version 2) RESULT 12

ID HSFLNG6PD standard; DNA; PRI; 219447 BP.

AC 144140;
DT 29-FEB-1996 (Rel. 47, Created)
DT 29-FEB-1996 (Rel. 47, Last updated, Version: 29-FEB-1996 (Rel. 47, Last updated, Version: DE Glucose-6-phosphate dehydrogenase (G6PD) generical and a gene; 219 gene; ABP-280 gene; actin-bind KW and a gene; G4B gene; BAB-280 gene; actin-bind KW and a gene; G4B ge Query Match 14.9%; Best Local Similarity 90.0%; Matches 261; Conservative partial, repeat\_region g ය 음 გ 용 გ გ g FFFFS

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repeat\_unit

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Medicine Washington University School of Medicine, St. Louis MO 63110 USA e-mail: ellson@genseq.apldbio.com and darids@genetics.wustl.edu Note: Gene predictions were accomplished with runs of Grail versions I. 1 and 1.2, coupled with fasta and blastx comparisons to genbank & non-redundant peptide libraries. Repeat analysis was accomplished via censor. NCBI gi: 1203968 Key Submitted by: Ellson Chen, Advanced Center for Genetic Technology, Applied Biosystems Division of Perlin Elmer Corp., 850 Lincoln Center Drive, Foster City, CA 94404 USA and David Schlessinger, glucose-6-phosphate dehydrogenase (GGPD) gene, complete cde's.

IA gene; 2.19 gene; ABP-280 gene; actin-binding protein;

DNase I-like protein gene; DNLIL gene; EMD gene; emerin;
emery-dreyfuss syndrome; filalani; FLN gene; G4.8 gene; G6PD gene; gdi gene; GdX gene; glucose-6-phosphate dehydrogenase;
P3 gene; CM gene; STA gene; XAP-1 gene; XAP-2 gene; XAP-7 gene; "Thirteen known and six candidate genes in 219.4kb of high GC DNA Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.N., Department of Molecular Microbiology and Center for Genetics in Eukaryota, Animalia, Metazoa, Chordata, Vertebrata, Mammalia, Theria, Eutheria, Primates, Haplorhini, Catarrhini, Hominidae Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D., Homo sapiens chromosome X region from filamin (FIN) gene to 29-FEB-1996 (Rel. 47, Created) 29-FEB-1996 (Rel. 47, Last updated, Version 2) /rpt\_family="Alu-Sp or Alu-Sq" /rpt\_family="Alu-J or Alu-S" 641..931 /rpt family="Alu-J or Alu-S" 1023..1313 between the human RCP/GCP and G6PD loci"; HSFLNG6PD standard; DNA; PRI; 219447 BP. /organism="Homo sapiens /evidence=EXPERIMENTAL /evidence=EXPERIMENTAL /evidence=EXPERIMENTAL /sequenced\_mol="DNA" 1..219447 /map="X" 226..503 /шар="Х" /map="X" Homo sapiens (human) Unpublished. repeat unit repeat unit repeat\_unit repeat unit D'Urso M.; 1-219447 L44140; source RESULT ò 

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Gaps

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Note: remainder of annotations omitted.

Query Match 14.9%; Best Local Similarity 90.0%;

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Matches

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7120 ttttttttttqagatggagtttcgctcttattgccgaggctggagtgcaatggcacaatct 7179

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Aug 27 08:17 US-08-231-565A-1 rge	/note="Pro-tRNA" /anticodon=(pos:unspecified,aa:Pro) +nun con 150		/anticodon-(pos:unspecified, aa:Val) BASE COUNT 242 a 296 c 333 g 300 t ORIGIN About 1 kb after segment 1.	Query Match 14.8%; Score 230; DB 58; Length 1171; Best Local Similarity 89.4%; Pred. No. 1.39e-99; Matches 261; Conservative 0; Mismatches 31; Indels 0; Gaps	Db 786 tttcttttgagatggggtttcgctcttgttgcccaagctggagtgcaatggagtgatctc 845	Qy 970 TITTTTGAGATGGAGTITCGCTTTTGTTGCCCAGGCTGGAGTGCAATGGCGCGATCT 102	846 ggctcacagcaacctccgctcccaggtccaagccattctcctgcctcaggctccggagt	Oy 1030 GGCTCACCATAACCTCCGGCTCCAGGTTCAAGCAATTCTCCTGCCTTAGCCTCGGTTAGGT 108  Db 906 aqctgggattacaggcataggcaccacagaccaggctaattttgtattttagtagagacg 965	Qy 1090 AGCTGGGATTACAGGCGTGCGCGCTATGCCTGATTTTGTAGTTTTTAGAGAGGC 114	<pre>Db 966 gagtttetecatgttggtcaggetggtetegaactecggacetcaggtgatecgcecace 102</pre>		Qy 1210 TCAGCCTCCCAAAGTGCTGGAATTACAGGCGTGAGCACCACGCCTGGCTGG	SUI	AC 20917) DT 08-FEB-1996 (Rel. 46, Created) DT 08-FEB-1996 (Rel. 46, Last updated, Version 1) DF Uman DNB commonce from cocmit 1.7468 Huntingford Disease Region.	DE chromosome 4p16.3 KW 4p16.3	OS Homo sapiens (human) OC Entaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;	ineila; butheria; riimates; hapiotnini; [1] [			KL enquires: numqueryesanger.ac.uk C IMPORTANT: C mits acquires: numqueryesanger.ac.uk		CC submissions. CC This sequence has been finished according to sequence map criteria CC This sequencing problems, CC as follows. An attempt is made to resolve all sequencing problems,	such as compressions and repeats, but not necessarily with annotated human repeat sequence elements (e.g. Alu). When	<pre>CC sequence is ambiguous, there is an annotation using the "unsure" CC feature key.</pre>
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08:17 US-08-231-565A-1.rge	34822, 3497635169, 3527135407, 3558635709, 3579835935, 3647336673, 3675736919, 3701137088, 3718137299, 37846.	37993, 3809038187, 3829138539, 4131941691)) /evidence=EXPERIMENTAL	/gone_x /map="x" /codom start=1 /function="binds actin"	/product="filamin" /db_xref="P1D:q1203969" /translation="MSSSHSRAGQSAAGAAPGGGVDTRDAEMPATEKDIAEDAPWKKI	remainder of annotations omitted.	Query Match 14.9%; Score 232; DB 10; Length 219447;	rvative 0; Mismatches 26; Indels 1; Gar	65611 agccgggcgtggtggctcacacctgtaattccagcacattgggaggctgaggcgggcaga 65670	65671 tcacctgaggtcaggagtttgagaccagcctgacca-cacggagaaaccctgtctctact 65729	99 TCACCTGAGGTCTGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCGGTCTGTACT 1140 80 aaaaatacaaaataagccagagatggtaggacatgctdtgatccgagtactcqqqaga 65789		5790 ctgaggcaggagaattgcttgaacccgggaggcagaggttgcactgagctgagatcgtgc 65849 	65850 catggcactccagcctgggcaacaagagggaactccatctcagaaaaa 65900	1019 CATTGCACTCCAGCCTGGGCAACAAAACGCAAACTCCATCTCAAAAAAA 969	14 HUMTGTPV2 1171 bp DNA PRI 14-JAN-1995		gssysts S transfer RNA-Pro; transfer RNA-Val. 2 of 2		E E		A human tRNA gene het	AL Gene 79 (2), 309-324 (1989) NE 90006760 NCBI qi: 339615	rce	/organism="Homo sapiens" tRNA 241312
Aug 27 08:17	Ħ	. E.E.E	FT FT	FT FT Q	Note: I	Quer) Best	Matches	Db 656 Cp 12	DP 656	Cp 1199 Db 65730	Ср 11	Db 65790 Cp 1079	DP 658	Ср 10	RESULT LOCUS	DEFINITION ACCESSION	KEYWORDS SEGMENT	SOURCE	ONG.	REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE COMMENT	FEATURES	Ŧ.

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The sequence from clone 1.174G8 has been finished in more than one

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1314 ctcggctcactgcaacctccggcgtccaagccattctcctgcctcagcctcctg 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                               The library was constructed using flow-sorted human chromosome 4 from a Hamster-Human hybrid cell line ( UV20H121-27 ) containing human chromosomes 4, 8 and 21.

VECTOR: scosl
L114G8 is contained in a clone contig spanning ~2MD which is described in Baxendale et al, Nature Genetics 4 ( 1993 ) 181-186. See also Myers et al, Cytogenet Cell Genet. 66 ( 1994 )
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1255..1546
/note="Alu repeat: matches 308..1 of consensus"
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                                                                                                      Human Genome Center, Los Alamos National Laboratory, NM 87545 under the auspices of the U.S. Department of Energy.
                             This sequence (L174G8C) is separated from the preceeding one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 230; DB 10; Length 1846;
Pred. No. 1.39e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 29; Indels
                                                      by a gap of about 1.2kb sized by restriction analysis. The true right end of clone L174G8 is at 1846. L174G8 is from cosmid library LA04NCO1 constructed at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1846 BP; 530 A; 440 C; 371 G; 505 T; 0 other;
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Best Local Similarity 89.9%;
Matches 259; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn Tue Aug 27 08:29:44 1996; MasPar time 130.22 Seconds 851.467 Million cell updates/sec

Tabular output not generated.

Run on:

(1-1559) from US08231565A.seq 1559 >US-08-231-565A-1 Title:

Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 91712 seqs, 35561689 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq23 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17

Mean 9.544; Variance 7.360; scale 1.297 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	0.00e+00	0.00e+00	2.45e - 170	3.98e-145	6,55e-106	1.04e - 96	1.04e - 96	₹	4.32e-95
Description	MART-1 melanoma antig	Tumour rejection anti	Tumour rejection anti	Tumour rejection anti	Human thymopoietin co	Human brain Expressed	Human brain Expressed	GDP-Fuc:beta-D-galact	DNA encoding a glycos
TD		T11550	976370	T11549	092779	059541	908650	013332	806950
88	17	11	12	11	15	œ	œ	7	6
% Query Match Length DB	1559	160	354	13585	6905	370	387	8174	8174
% Query Match	100.0	40.6	22.5	19.5	14.9	13.8	13.8	13.6	13.6
Score	1559	633	350	304	232	215	215	212	212
Result No.	1	2	m	4	0	9	7	<b>∞</b>	6

4.32e-	2.16e-92	7.47e-	by 2.59e-91		m	ge 3.70e-89	hae 3.70e-89	m	÷	÷	1.28e-88	5.27e-87	5.27e-87	6.28e-86	Ξ.	_		2	•	2.58e-		8.89e-	3.06e-	3.06e-	3.63e-	3.63e-	1.06e-	1.25e-	g 4.	4.	4.31e - 81	4.31e-
Genomic sequence enco Complete genomic sequ	MIP-1-alpha.	BSSL/CEL Gene.	AP2 sequence obtd. h	Human brain Expressed	hML genomic DNA.	tin	Sequence encoding ha	Human thrombopoietin	Sequence of human pul	Genomic clone encodin	HSA gene.	TXA2 receptor gene.	c-fos gene.	Human Cdn-2 DNA.	Human FcERI beta chai	Clone of recombinant	A4 amyloid precursor	Human thrombopoietin	Sequence encoding hae	Tumour rejection anti	Human centromeric seq	Serglycin - proteogly	Oncogene R-ras mutant	hML genomic DNA.	Human brain Expressed	Neural thread protein	Human thymopoletin co	AP1 sequence obtd. by	Human IL-1 receptor	cDNA of human interle	IL-1R cDNA.	hOP1 human osteogenic
N81564 N70102	085367	054222	063862	059876	094109	092781	T04051	T03943	N80643	N80616	036952	025388	063815	095493	051024	046852	011434	T03943	T04051	T11549	Q20240	044278	T08553	094109	061222	977874	092779	063859	073764	N90118	049933	972708
	H	11531 9	283 11	257 8				4823 17	10475 2	10475 1	19012 6	2932 4	6210 11	6511 15	11357 9	13104 8	3804 2	4823 17	4823 17	13585 17	13875 4			7849 16		1479 13		Ţ	2600 13	2600 1	2963 8	17350 12
13.6 13.6	13.3	13.2	13.1	13.0	13.0	12.9	12.9	12.9	12.8	12.8	12.8	12.6	12.6	12.5	12.5	12.5	12.4	12.4	12.4	12.3	12.3	12.3	12.2	12.2	12.1	12.1	12.1	12.0	11.9	11.9	11.9	11.9
212 212	207	506	202	203	203	201	201	201	200	200	200	197	197	195	195	195	193	194	194	192	192	191	190	190	188	188	189	187	186	186	186	186
10 11	12	13	14	15	16	11	18	19	20	21	22	23	24	52	56	27	88	59	30	31	35	33	34	32	36	37	38	39	40	41	42	43
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## ALI GNMENTS

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<b>≿</b>	1501	ATCATAAAGGATCAGAGATTCTGAAAAAAAAAAAAAAAA	٠,
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tumour; treatment; detection; vaccine; HLA-A2; adoptive transfer,

Homo sapiens 25-JAN-1996. diagnosing melanoma

WPI; 96-097390/10.

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Best Local Similarity

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Sequence Query Match

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ö for therapy of disorders characterised by the expression of the tumour processed to a tumour rejection antigen presented by HIA-A2 molecules. 540 707 541 GIGTTAAAATTTTAGTAGGTCCGCTAGCAGTACTAATCATGTGAGGAAATGATGAGAAAT 600 This sequence encodes the tumour rejection antiqen precursor which is 54 ATGCCAAGAGAAGATGCTCGCTTCATCTATGGTTACCCCAAGAAGGGGCACGGCCACTCT 113 120 114 TACACCACGCTGAAGAGGCCGCTGGGATCGGCATCCTGACAGTGATCCTGGGAGTCTTA 173 9 tumour rejection antigen may be used for diagnosis or in vaccines or Gaps used for developing prods. for diagnosis or treatment of expression sequence was isolated from the melanoma cell line, LB-39-MEL. The gtgttaaaaattttagtaggtccgctagcagtactaatcatgtgaggaaatgatgagaaat tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 481 TCTAATGTTCTCCTTTGGAATGGTGTAGGAAAATGCAAGCCATCTCTAATAATAAGTCA Tumour rejection antigen; precursor; HLA-A2 molecule; tyrosinase; isolation; melanoma; cell line; LB-39-MEL; diagnosis; vaccine; 1 atgcgaagagaagatgctcacttcatctatggttaccccaagaagggggacggccactct Nucleic acid coding for a tumour rejection antigen precursor - is .; 0 The tumour rejection antigen is not related to tyrosinase. Length 354; 2; Indels ပ 83 T; 708 attaaattgggaaaactccatcaataaatgttgcaatgcatgata 752 Traversari

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Length 13585;

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3.19 US-08-231-565A-1 mg	ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaa 	agtcttcatgttggcattcaatgtgccttaacaagaagatgcccacaagaaggtttgat 	catcgggacagcaaagtgtctcttcaagagaaaaactgtgaactgtggttcccaatgct 	ccactfgcttatgagaaactctctgcagaacagtcaccaccaccttattcacct 354 	standard; 1996 (fi rejection rejection treatmen T lympho	Key Location/Qualifiers misc_feature 2685 /*tag= a /note= "Unidentified nucleotide." misc_feature 94229456	* ~ ~ ~	c "Unidenti 157-A1. 11996. 11995; U08- 11994; US- 11995; US-	(LUDW-) LUDWIG INST CANCER RES.  Boon-falleur T, Brichard V, Coulie P, De PLAEN E;  Traversari C, Van PEL A, Wolfel T;  WFI; 96-091390/10.  Genomic DNA encoding a tumour rejection antigen precursor - processed to antigen presented by HLA-A2, useful for treating or	diagnosing melanoma Claim 3; Page 18-22; 41pp; English.  Claim 3; Page 18-22; 41pp; English.  The timour rejection antigen (TRA) presented by HIA-A2 molecules. TRA is used to generate cytotoxic T lymphocytes for treating cancer (esp melanoma). It can also be used to raise specific antibodies, and when complexed with HIA-A2, it can be used to prduce vaccines. Cytotoxic T lymphocytes so generated can be used in adoptive transfer or generated, or they can be generated in vivo by using a vector containing the appropriate gene or using TRA or TRAP together with an adjuvant that facilitates entry into HIA-A2 presenting cells. Diagnostic methods involving the detection of expression of TRAP can be used in the detection of cancers.  Sequence 13585 BP; 3827 A; 2859 C; 2968 G; 3894 T;
Aug 27 08:19	121 174	181	241	301	111549 T11549; T11549; 18-APR- Tumour Tumour; T cell; Homo sa	Key misc_fe /*tag= /note= misc_fe	/ reag= /note= but the deduced	/*tag= /note= W096015 25-JAN- 27-JUN- 08-JUL- 10-JAN-	(LUDY Boon- Trave WPI; Genom	diagnosi Claim 3; The tumour r is used melanoma when com Cytotoxi transfer vector c with an Diagnost can be u
Au	e S	දු දු	do y	g &	RESULT ID T AC T AC T DT 1 DT 1 DE T KW T KW T KW T COS H	HLLLLL	FFF	FT PN PR PR	PA PI PI PT	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

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ï on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue TTTTTGAGATGGAGTTTCGCTTTTGTTGCCCAGGCTGGAGTGCAATGGCGGATCTTGGC 1032 240 12] atgcgccactaccccag-ctaattttgtattttnagtagagatggggtttctccatgttg 179 61 tcaccgcaacctccgcctcccgggttcaagcgattctcctgcctcagcctcccaagtagc 120 180 for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes 9 Gaps type, and for prepn, of antisense sequences, probes and constructs. EST01548 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also 059041-061440. Sequence 387 BP; 88 A; 104 C; 89 G; 105 T; library as part of a large set of ESTs which can be used as markers 121 tgggattacaggcaccaccacgcctggctgattttntatttttagtagacacgggt 1 gtttcgctcttgttgcccaggctggagtgcaatggcgcaatctcgactcaccacaacctc transcription; mapping; locations; chromosomes; chromosomal; ss. Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging The Expressed Sequence Tag was isolated from a human brain cDNA 1, Gene transcription product; genetic markers; tagging; in vivo; 13.8%; Score 215; DB 8; Length 387; 90.7%; Pred. No. 1.04e-96; 0; Mismatches 24; Indels 1213 GCTCCCAAAGTGCTGGAATTACAGGCGTGAGCCACCACCACCTGGC 1258 241 acctcccaaagtgctgggattacaggcgtgagcacttgcgcctggc 286 Human brain Expressed Sequence Tag EST01548. 12-FEB-1993; U01294. 12-FEB-1992; US-837195. (USSH ) US DEPT HEALTH & HUMAN SERVICE. Example 4; Page 234; 500pp; English. Adams MD, Moreno RF, Venter CJ. WPI; 93-272882/34. BP. Best Local Similarity 90.7%; Q59806 standard; cDNA; 387 (first entry) 244; Conservative of most human genes Homo sapiens. 16-MAR-1994 W09316178-A. 19-AUG-1993. Query Match 059806; 1033 973 181 Matches

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36;

Length 370; Indels

Score 215; DB 8; Pred. No. 1.04e-96; 0; Mismatches

13.8%; 87.4%;

250; Conservative

Best Local Similarity

Query Match Matches

8 Gaps

1 tttttgagacggagtttcactcttgttgcccaggctggagtgcaatggcatgatctcggc

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	Aug 27 ts: 19	U3-Ua-231-303A-1:mg
CC disorders, CC the DNA can SQ Sequence	rs. The protein and can be used in gene e 6905 BP; 2028	the DNA can be used as diagnostics; therapy. A; 1280 C; 1359 G; 2238 T;
Query Match Best Local S Matches 26	th 14.9%; Similarity 90.0%; 261; Conservative	Score 232; DB 15; Length 6905; Pred. No. 6.55e-106; 0; Mismatches 29; Indels 0; Gaps 0;
Db 6172 gc       Cp 1258 GC	cogggogcagtggctcacgcc 	geogggogaatiggatcaogcotgtaatcecagcactttgggaggocgaggoggagt 6231 
Db 6232 ca       Cp 1198 CA	cctgaggtccggagttcgag 	cactgaggtccggagttcgagacgagcctgaccaacatggagaaacctgtctctacta 6291 
Db 6292 aa     Cp 1138 AA	aatacaaaattagccaggca                ACTACAAATTAGTCAGGCA	aaaatacaaaattagccaggcatggtggtgcatgcctgtaatcctagctactccggaggc 6351 
Db 6352 tg       Cp 1078 TA	aggcaggagaatcgcttgaa 	tgaggcaggagaatcgcttgaaccttggaggegaggttgctgtgagccgagatcgcgcc 6411 
Db 6412 at       Cp 1018 AT	.tgcactctagcctgggcaac 	attgcactctagcctgggcaacaagaggaaactctgtctcaaaataaa 6461 
RESULT 6  Q59541 standa  Q59541; DT 16-WAR-1994 DE Human brain E WW Gene transcription OS Homo sapiens. PN W03316178-A. PN W03316178-A. PR 12-FEB-1993; PR 12-	The following the following standard; cDNA; 370 BP.  16-MAR-1994 (first entry)  16-MAR-1994 (first entry)  16-MAR-1994 (first entry)  16-MAR-1994 (first entry)  18-MOSCIPION; mapping; locations; chromosom  18-MOSJ8[178-A.  19-KEB-1993; U01294.  12-FEB-1993; U01294.  16-FEB-1993; U01294.  17-FEB-1993; U01294.  18-FEB-1993; U01294	T 6 09541 standard; CDNA; 370 BP. 059541; 16-WAR-1994 (first entry) 16-WAR-1995 (dene transcription; mapping; locations; chromosomes; chromosomal; ss. 16-WAG-1993. 12-FEB-1992; US-837195. 18-FEB-1992; US-87195. 18-FEB-1992; US-982;

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à	1106 GTGGGCGACTATGCTGACTATTTGTAGTTTTAGTAGAGGGGGTTTCTCCATGTTG 1165	Db 4247 cttggcctcccaaagtgctgggattaca
qo o	180 gtcaggctggtcttgaactcctgacctcaggtgatccgcctgcct	Qy 1209 CTCAGCCTCCCAAAGTGCTGGAATTACA
<u>.</u> 49	240 ctaqqattacaqqcataaqccactqcqcc 268	RESULT 9 ID 056908 standard; DNA; 8174 BP.
à	1226 CTGGAATTACAGGCGTGAGCCACCGCC 1254	
		E DNA encoung a giycosyltransieras KW Glycosyltransferase; fucosyltrans
RESULT ID Q	LT 8 Q13332 standard; DNA; 8174 BP.	surface; oligosa Homo sapiens.
AC Tu	013332; 07-MOV-1001 (first entry)	FH Key Location/Qualifie
E i	OP-NOV-1991 (1118) entry) GDP-Pucibeta-D-galactoside alpha(1,2)-fucosyltransferase gene.	/*tag= a
ž ć	Glycosyltransferase. Homo saniens	PN W09402616-A. PD 03-FFR-1994.
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<u>.</u> E	CDS 46863/83 , , , , , , , , , , , , , , , , , , ,	VINU ( IMNU)
NA Ca	W09112340-A.	PI Lowe JB; np wpr: 94-048874/06
	22-R03-1991. 14-FBB-1991; U00899.	
R G	14-FEB-1990; US-480133,	
R R	14-FEB-1990; US-479858. 12-DEC-1990; US-627621.	FI Vitro reactions to modify cell su PT blood qp. determinants, to protec
PA		
I e	Lowe JB;. wpr. 01-24715/24	
5 E	P-PSDB; R13751.	
PT	ne conveying post-translational charac	_
PT	e.g. the presence of soluble or membrane bound oligo or polysaccharide or qlycosyltransferase.	CC See also Q56905-12. SQ Sequence 8174 BP; 1628 A;
PS	Disclosure; Fig 3, 155pp; English.	
ဗ	The DNA encodes a protein sequence capable of functioning as a GDP— Fnc:[heta=D-Ga] alpha(1.2)— fncosvltransferase. The sequence	Query Match 13.6%; Score Rest Local Similarity 86.6%; Pred.
88	coded by nucleotides 4782 - 5780 represents the functional protein.	
ខ្លួ	The enzyme produced by the DNA sequence can be used in enzymatic fucogulation of chain-ferminating galactose regidues on lactose-	Db 4007 tttttttggagacggagttcactct
8 8	amine or neolacto type beta-D-galactoside to alpha-2-L-fucose	
ខ្ល	residues. See also 013330-013333.	Qy 969 TTTTTTTTGAGATGGAGTTTCGCTTTT
ò	Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T;	Db 4067 caqetcaccqcaactecqcecccqqq
õ	Query Match 13.6%; Score 212; DB 2; Length 8174;	
¥ ₩	Best Local Similarity 86.6%; Pred. No. 4.32e-95; Matches 251; Conservative 0; Mismatches 39; Indels 0; Gaps 0;	Qy 1029 TGGCTCACCATAACCTCGGCCTCCCAGG
ź	230V + ++++++++++++++++++++++++++++++++++	Db 4127 tggctgggattacaggcattgcgccacca
3	400/	Qy 1089 TAGCTGGGATTACAGGCGTGCGCCACTA
δ	969 TTTTTTTTTGAGATGGAGTTTCGCTTTTGTTGCCCAGGCTGGAGTGCAATGGCGCGATCT 1028	Db 4187 aggetttetecacgttggteaggetggt
g g	4067 cageteacegeaactecegecececegggtteaggegatteteetgeeteageeteeggg 4126	- - - - - - - - - - - - - - - - - -
δy	1029 TGGCTCACCATAACCTCCCGCGTTCCAGGTTCTCCTGCCTTAGCCTCTGAG 1088	
QQ	4127 tggctgggattacaggcatgcgccaccatgcccggctaattttgtattttaagtagac 4186	
δ	1	Qy 1209 CTCAGCCTCCCAAAGTGCTGGAATTACA
q	4187 agggitteteeacgitagicaggeitagieteeaaciteeaaciteeaaciteaaciteaacitaateeacec 4246	BESULT 10
ì	- 1	N815
Ž	0031	DT 05-DEC-1990 (first entry)

Db 4247 cttggcctcccaaagtgctgggattacaggtgtgagccaccgcgcctggc 4296		ひかつ しじじきししじん かんしゅうしき かんきししじしん かんきゅう しゅうしゅん かんしん しゅうしゅう しゅう
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closure; Fig 3; 249pp; English.
sequence is that encoding human glycosyl transferase. The enzyme duced by the DNA may be non glycosylated. This prevents premature s of enzyme activity. It can also be used in in vitro reactions to also 25,005-12. cagctcaccgcaactcccgcccccgggttcaggcgattccctgcctcagcctcccgag 4126 7 agggtttctccacgttggtcaggctggtctcgaactcccaacctcaggtgatccaccac 4246 7 ttttttttggagacggagtttcactcttgttgcccaggctggagtgtaatggcatgatct 4066 TGGCTCACCATAACCTCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTTAGCCTCGTGAG 1088 9 GGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATCTGCCCGC 1208 0; Mismatches 39; Indels 0; Gaps oosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell; face; oligosaccharide; ss. fragment encoding a glycosyltransferase - can be used for in ro reactions to modify cell surface oligosaccharide(s) e.g. od gp. determinants, to protect against transplant rejection 1996 T; cttggcctcccaaagtgctgggattacaggtgtgagccaccgcgcctggc 4296 Match 13.6%; Score 212; DB 9; Length 8174; ocal Similarity 86.6%; Pred. No. 4.32e-95; 2322 G; 2228 C; Location/Qualifiers 4686..5783 encoding a glycosyltransferase. 1628 A; 9 908 standard; DNA; 8174 BP. (first entry) s 251; Conservative -JUL-1993; U06703. -JUL-1992; US-914281. NMI ) UNIV MICHIGAN. 94-048874/06. 3DB; R45936. ag= a 402616-A. sapiens JUL-1994 EB-1994. nence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                 the introns removed then is joined to a cDNA clone. The desired genomic:cDNA is then generated by looping out of unwanted sequences using oligonucleotide-directed deletion mutagenesis. The protein
                                                                                                                                                                                                                                                                                                                                               Disclosure; p; English.
In the construction of the full length protein C gene this sequence
                                                                                                                                                                                                                                                                                                                                                                                                      recombinant DNA, has substantially the same biological activity as natural protein C and is hence useful in the treatment of blood
                                                                                                                                                                                                                                                                                                                                                                                            produced upon transformation of mammalian host cells, contg. the
                                                                                                                                                                                                                                                                                                                                                                                                                                 2605 T;
                                                                                                                                                                                                                                                                                                                             Protein C DNA coding sequence and expression vector for prodn. used for treating blood coagulation disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.6%; Score 212; DB 1; Length 1171
Best Local Similarity 87.5%; Pred. No. 4.32e-95;
Matches 253; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 3292 C; 3375 G;
Genomic sequence encoding protein C.
Human protein C; blood coagulation disorders; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                       coagulation disorders. See also N81563. Sequence 11715 BP; 2443 A; 3292
                 Location/Qualifiers
2131..2200
                                                                                                                                                                                                                                                                                                  Foster DC, Murray MJ, Berkner KL.;
                                                                                                                                                                                                                         10517..12006
                                                                                                            5212..5349
                                                      3464..3630
                                                                                5093..5117
                                                                                                                                        5452..5586
                                                                                                                                                                   8255..8397
                                                                                                                                                                                              9270..9387
                                                                                                                                                                                                                                                                                         (ZYMO-) Zymogenetics Inc.
                                                                                                                                                                                                                                                                      28-OCT-1987; 309528.
29-OCT-1986; US-924462.
                                                                                                                                                                                                                                                                                                           WPI; 88-121259/18.
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/label=exon VII
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/label=exon II
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to 136"

US-08-231-565A-1 mg Aug 27 08:19

human Protein C; anti-coagulant; thrombosis; serine protease; ss. Complete genomic sequence of human Protein C. amino acids -19 to +37" 3631..5092 /note= "encodes amino acids -42 to -20" to 45" 91 Location/Qualifiers 2131..2200 amino acids 46 to amino acids 38 .T 11 N70102 standard; DNA; 11724 BP 2201..3463 5348..5449 2464..3630 5093..5117 5118..5209 (first entry) 5210..5347

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US-08-231-565A-1 mg

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6434 teteageteaceacaaceteegeeteetggatteaagegatteteetgeegeageeteee 6493 1026 TCTTGGCTCACCATAACCTCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTTAGCCTCCT 1085 6494 gagtagctgggattacaggcatgcgccaccacgcccagctaattttgtgtttttagtaga 6553 6374 tcttttttttgagatggagtttcactcttgttgtcccaggctggagtgcaatgacgtga 6433 967 TCTTTTTTTTGAGATGGAGTTTCGCTTTTGTTG-CCCAGGCTGGAGTGCAATGGCGCA 1025 gaaggggtttctccgtgttggtcaagctggtcttgaactcctgacctcaggtgatccacc 6613 0; Mismatches 35; Indels 1; Gaps used as a hybridisation probe. The remainder of the coding sequence peptide and the forst 23 amino acids of protein C was isolated and protein C. A cDNA which lacked the coding sequence for the pre-pro was obtained from a human genomic DNA library in lambda Charon 4A. Recombinantly produced protein C can be used to treat thrombotic Ë Human protein C or activated protein C - prepd. using expression A lambda gt cDNA library was prepared from human liver mRNA. The library was screened with iodine-125 labelled antibody to human 2607 / Match 13.6%; Score 212; DB 2; Length 11724; Local Similarity 87.5%; Pred. No. 4.32e-95; 1206 CGCCTCAGCCTCCCAAAGTGCTGGAATTACAGGCGTGAGCCACACGCC 1254 6614 tgccttggcctcctaaagtgctgggattacaggcgtgagccaccgcgcc 6662 vector capable of integration in mammalian host cell DNA 3370 G; 3302 C; Murray MJ, Berkner KL, Foster DC, Davie EW. WPI; 87-081505/12. /note= "encodes amino acids 224 to 419" disorders such as venous thrombosis. Claim 2; Page 33; 52pp; English. 2445 A; 10515.,11104 11151..11156 11380..11385 (ZYMO-) ZYMOGENETICS INC. (UNIW ) UNIV OF WASHINGTON. 253; Conservative US-749600. 27-JUN-1985; US-749600 15-AUG-1985; US-766109 11724 BP; 26-JUN-1986; 304970. P-PSDB; P70855. polyA signal polyA\_signal EP-215548-A. /\*tag= q polyA\_site 25-MAR-1987 /number= 8 polyA site /number= 7 CO c 0 Sequence Query Match /\*tag= /\*tag= /\*tag= /\*tag= \*tag= Matches exon 6554 셤 셤 ð ð 염 ð 염 g Š à

Q85367 standard; cDNA; 4788 BP.

RESULT ID Q8

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The primers (054223-28) are used to amplify fragments of the BSSL / CEL gene, (054222). Which encodes a bile salt-stimulated lipase / carboxyl ester lipase which when expressed by transgenic animals can be used as a human milk substitute. The BSSL is designed to pass through the stomach and is activated in the small intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           As it has a broad substrate specificity it can mediate the complete digestion of most dietary lipids. 3527 C; 3280 G; 2260 T; Sequence 11531 BP; 2464 A; 3527 C; 3280 G; 2260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed by transgenic non-human mammals and used as human milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding bile salt-stimulated lipase/carboxyl ester lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlsson PNI, Enerback CSM, Hansson SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toernell JBF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 206; DB 9; 1
Pred. No. 7.47e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substitute, contains intron sequences Claim 1; Page 43-51; 76pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 10650..11490
                                                                                                                                                                                                                                                                                                                                      11491..11531
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Best Local Similarity 86.0%;
         1653..11397
                       /*tag= a
/product= BSSL/CEL_protein
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                                            1..1640
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19-MAR-1993; SE-000902.
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23-DEC-1993.
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0; Gaps

0; Mismatches 40; Indels

Matches 246; Conservative

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5237 ggcgcggcggctcacctctgtaatcccagcacgttgggagcccaaggtgggtagatcacc 5296

; 5416 CCAGGAGAATTGCTTGAACCTGGGAGGCGGAGGTTATGGTGAGGCCAAGATCGCGCCATTG 1015 1254 GCCCTGCTGCTCACGCCTGTAATTCCAGCACTTTGCGAGGCTGAGGCGGGCAGATCACC 1195 66 tgaggtcaggagttcaagaccagcctggccaacatggtgaaacccgtctctactaaaaa 125 ggcaggagaatcgcttgaacccgggaggtggaggttgcagtgagccgagatcgccact 245 Gaps gcaggagaatcgcttgaactcaggaggcggaggttgcggtgagccgagatcatgccactg detect insertions or deletions in DNA sequences. Such mutations a markers of cancer so such primers can be used in the diagnosis of 5297 tgaggtcaggagtttgagaccagcctgactaaaatggagaaacctcttctctactaaaaa tacaaaattagccaggcgtggtggcgcttgcctgtaatcccagctactcgggaggctgag Arbitrary primers; AP-PCR; amplification; tumour cells; cancer; Identification of tumour cells - by analysing DNA to determine whether insertions or deletions have occurred in reiterated Disclosure; Page 52; 67pp; English. The sequence was obtd. by PCR with arbitrary PCR primers used 2; Length 283; 0; Mismatches 30; Indels cancer, esp. colorectal, stomach or pancreatic tumours. See also Q63837-63. 49 T; Peinado MA; AP2 sequence obtd. by PCR for tumour specific DNA. Query Match 13.1%; Score 205; DB 11; Best Local Similarity 88.5%; Pred. No. 2.59e-91; 94 G; (CALB-) CALIFORNIA INST BIOLOGICAL RES Mcclelland M, 77 C; JT 14 Q63862 standard; cDNA; 283 BP. 63 A; 247; Conservative (first entry) insertions; deletions; ss. Ionov Y, Malkhosyan S, 26-MAY-1994. 12-NOV-1993; U10904. 13-NOV-1992; US-975737. Welshi; 283 BP; WPI; 94-183529/22 29-JAN-1995 W09411531-A. Perucho M, Synthetic. sednences Sequence 063862; Matches 5357 5417 1074 1134 186 RESULT გ g 염 g 음 g 9 g 유 გ 용 염 g 셤 g 염 

1075 GGCAGGAGAATTGCTTGAACCTGGGAGGCGGAGGTTATGGTGAGCCAAGATCGCGCCATT 1016

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      987 TTTCGCTTTTGTTGCCCAGGCTGGAGTGCAATGCCGCGATCTTGGCTCACCATAACCTCC 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 tgtnccaccacgcctggctaattttnta-tttaagtagagatggggtttctccatgttgg 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                teagtetggteteaaactectgaecteaggtgatetggeeaecteggeetecaaagtge 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tttccctctcgttgcccaggctggagtgcaatggcgtnatcttagctcaccacaacctct 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library as part of a large set of ESTs which can be used as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for human genes transcribed in vivo. They can be used to facilitate
                                                                                                                                                                                                                           transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               markers for human genes transcribed in-vivo, facilitate tagging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Expressed Sequence Tag was isolated from a human brain cDNA
                                                                                                                                                                                                       Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                            Enriched oligonucleotides and corresp. sequences - used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.0%; Score 203; DB 8; Length 257; Best Local Similarity 89.5%; Pred. No. 3.10e-90; Matches 231; Conservative 0; Mismatches 26; Indels
246 gcactccagcctgggcgacaga-gcgagactccgtctca 283
                                       1015 GCACTCCAGCCTGGGCAACAAAAGCGAAACTCCCATCTCA 977
                                                                                                                                                                                  Human brain Expressed Sequence Tag EST01565
                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 246; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Adams MD, Moreno RF, Venter CJ.
                                                                                                     JT 15
Q59876 standard; cDNA; 257 BP.
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W09316178-A.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols MPsrch tpn

Tue Aug 27 18:37:02 1996; MasPar time 260.36 Seconds 1033.428 Million cell updates/sec Tabular output not generated. Run on:

1 ATGCCHMGNGARGAYGCNCA......SNCCNCCNCCNTAYWSNCCN 354
TACGGNKCNCTYCTRCGNGT.......wnGGNGGNGGNATRSWNGGN (1-118) from US08231565A.pep 1420 >US-08-231-565A-2 Description: Perfect Score: N.A. Sequence: Title:

Comp:

TABLE bktranslate2 Scoring table:

Gap 30

Dbase 0; Query 0 STD: Nmatch

270440 seqs, 380027776 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

embl-new3 Database:

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLIN 9:PR11 10:PR12 11:PR0 12:ROD 13:SYN 14:UNC 15:VRT 16:VIR1 17:VIR2

genbank92 Database:

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5 32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG 39:PLM1 40:PLM2 41:PLM3 42:PLM4 43:PLM5 44:PLM6 45:PLM7 46:PLM8 47:PR11 48:PR12 49:PR13 50:PR14 51:PR15 52:PR16 53:PR17 54:PR18 55:PR19 56:PR110 57:PR111 58:PR112 59:PR113 60:RD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6 66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3 73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

90:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PLN 86:PRI 87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT u-emb145 92 genbank-new1

Database:

Database

93:part1

Mean 63.591; Variance 167.878; scale 0.379 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

# US-08-231-565A-2.rgc Aug 27 18:29

and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.		1.18e - 183	8	9.32e - 04	3.52e-01		2.58e+00			-			3.21e+00	7.52e+00	-:				•	9.28e+00	•	9.28e+00	9.28e+00	•	9.28e+00	1.41e+01	1.14e+01	1.41e+01	1.41e+01	1.14e+01	•	•	2.6le+01	•	•	•		•	•		•	•	2.61e+01	2.61e+01	2.61e+01	3.19e+01
Description		Human differentiation	Human melanoma antige	manganese superoxide		H.sapiens SOD-2 gene	the ic	pira hardjo	H. sapiens gene for gl	Chironomus tentans Ba	Gallus gallus transfo	B.rerio Notch mRNA.	Caenorhabditis elegan	L.borgpetersenii IS-l	Herbaspirillum serope	rearranged	ы	cunic	O.cuniculus mRNA for	Trichoplusia ni granu	Pseudalatia unipuncta	Pseudalatia unipuncta		Oryctolagus cuniculus	Caenorhabditis elegan	B.napus mRNA for poly	lis beta-	aegypti 1	(c)	Synechocystis sp. slr	Leptospira borgpeters	C. jacchus SRY gene.	(tro	s gen			Erigeron hybridus chl	Haplocarpha scaposa c	Arctotis stochadifoli	A.vinelandii nitrogen	Homo sapiens (subclon	H.sapiens ENO3 gene f	endai virus (s	S.erythraea second an	erythraea ery	Caenorhabditis elegan
a		HSU06654	HSU06452	S77127	ACU12386	HSS0D2G	A21548	LEPREPEL	HSGLARS09	CTBR21	CHKTGFBA	BRNOTCH	CELF47F2	LBISLIKE	HEUNIFABX	OATCVG6	OATCCG4	RABRBAT	OCRBATPRO	GVTVEF	BAUGVEP	UGVEP	UGVEP	RABMEMGLY	CELC18A11	BNPGALACR	POABETA2	AAU02548	MOSVITE	SYCSLRD	LEP IS1533	CJDNASRY	TRNTETE	XLTF3A36	LEPOOXE	S40548	EGOCPNDHF	HAYCPNDHF	ARZCPNDHF	AVINIFANFA	HUM23DC1Z	HSEN03	PAMFHNL	SERERYAB	SEERYABS	CEM03C11
DB		52	25	59	27	25	36	22	20	28	11	11	28	22	22	34	34	34	34	11	16	16	16	34	27	œ	42	27	31	56	22	47	56	6	41	43	40	41	39	18	53	20	75	52	25	4
Length	, !	752	1524	12857	41591	6004	1467	1467	267	1384	3347	7471	24537	1458	3287	708	167	2208	2254	3556	3572	3572	3572	3934	43449	1599	2121	6504	8780	110908	1477	684	830	1337	2074	2146	2214	2226	2226	2772	4032	7194	10603	20235	20444	40780
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Score		1392	1392	172	147	142	138	138	137	137	137	137	137	133	133	132	132	132	132	132	132	132	132	132	132	130	131	130	130	131	128	127	127	126	127	127	127	127	127	127	126	127	127	127	127	126
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# ALI GNMENTS

HSU06654 752 bp mRNA PRI 30-JUL-1994 Human differentiation antigen melan-A protein mRNA, complete cds. U06654 Homo sapiens g517022 human. ORGANISM DEFINITION ACCESSION KEYWORDS SOURCE

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REFERENCE AUTHORS

JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL

COMMENT FEATURES

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Eucarvotae; Metazoa; Chordata; Vertebrata; Cnathostomata; Mammalia;	···
Eutheria; Primates; Catarrhini; Hominidae; Homo.	Db   401 categggacagcaaagtgtetettcaagagaaaaaetgtgaaectgtggtteceaatget 460
AUTHORS Coulie, F.G., Bricht, V., Van Pel, A., Wolfel, T., Schneider, J., Traversari, C., Mattei, S., De Plaen, E., Lurquin, C., Szikora, J.P.,	Qy 241 CAYMGNGAYWSNAARGTNWSNYTNCARGARAARAAYTGYGARCCNGTNGTNCCNAAYGCN 300
Renauld, J. and Boon, T. TITLE A new gene coding for a differentiation antigen recognized by autologous cytolytic T lymphocytes on HIA-A2 melanomas [see	Db 461 ccacctgcttatgagaaactctctgcagaacagtcaccaccttattcacc 513
comments] JOURNAL J. Exp. Med. 180, 35-42 (1994) MEDITAE 94275389	RESULT 2
	TION
TITLE Direct Submission JOURNAL Submitted (11-FEB-1994) Pierre Coulie, Ludwig Institute for Cancer Research, Brussels Branch, Avenue Hippocrate 74, UCL 7459.	ACCESSION U06452 NID 9476131 KEYWORDS ,
Brussels, B-1200, Belgium	SOURCE human. ORGANISM Homo sapiens
FEATURE SOLUCE 1.752	
	REFERENCE 1 (bases 1 to 1524) AUTHORS Kawakami,Y., Eliyahu,S., Delgado,C.H., Robbins,P.F., Rivoltini,L.,
/number=1 exon 136237	Topalian, S.L., Miki, T. and Rosenberg, S.A. TITLE Cloning of the gene coding for a shared human melanoma antigen
/number=2 CDS 161517	
/note="NCBI gi: 517023" /codon_start=1	
/ produce="metan-A protein" / db_xref="metan-A protein" / db_xref="ptD:g51-7023"	AUTHON AMAKAMI, TAKAKAMI, TITLE Direct Submission TITLE Direct Submission JOORNAL Submitted (08-FEB-1994) Yutaka Kawakami, Surgery Branch, National
CWYCRRRNGYRALMDKSLHVGTQCALTRRCPQEGFDHRDSKVSLQEKNCEPVVPNAPP AYEKLSAEQSPPPYSP"	
exon 238334 // number=3	COMMENT NCBI gi: 4/6131 FEATURES Location/Qualifiers
exon 335448 // // // // // // // // // // // // //	source 11524 /organism="Homo sapiens"
exon 449752 /number=5	/cell_line="melanoma cell line, 501mel" /tissue type="melanoma"
polyA_signal 730735 polyA_site 752	CDS 54410 / / / / / / / / / / / / / / / / / / /
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Matches $207_i$ Conservative 81; Mismatches $65_i$ Indels $0_i$ Gaps $0_i$	AYEKLSAEQSPPPYSP" BASE COUNT 435 a 330 c 324 g 435 t
161 atgccaaqagaaqatgctcacttcatctatggttacccaaqaaqggggacqgccactct 220       :    :  :     :  :  :  :      :     :     :	:
ATGCCNYGNGARGA YGCNCAYTTYATHTAYGGNTAYCCNAARAARGGNCAYGGNCAYWSN	atch ge.0%; Score 1392; DB 52; Length 1524; cal Similarity 58.6%; Pred. No. 1.18e-183;
22) tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 280   :                 :                 :	Matches 207; Conservative 81; Mismatches 65; Indels 0; Gaps 0; Db 54 atgoccaaqaqaaqatgotcacttcatctatqqttaccccaaqaaqqqqcacqqccactct 113
ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttga	
:  :      :      :	Db   114 tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 173
agtottoatgttggcactcaatgtgcottaacaagaagatgcccacaagaag :::   :           :  :   :     :	
181 WSNYTNCAYGTNGGNACNCARTGYGCNYTNACNMGNMGNTGYCCNCARGARGGNTTYGAY 240	Db 174 ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaa 233

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S77127 12857 bp DNA PRI 26-SEP-15 manganese superoxide dismutase/MnSOD [human, embryoniclung fibroblast cell line W138, Genomic, 12857 nt].

DEFINITION

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Editing of transfer RNAs in Acanthamoeba castellanii mitochondria Science 259 (5096), 812-816 (1993) H(+)-transporting ATPase subunit 1; NADH dehydrogenase subunit 1; 235-like ribosomal RNA; YMF46; YMF47; YMF48; Ile-tRNA; Ala-tRNA; Pro-tRNA; Asp-tRNA; initiator Met-tRNA; 165-like ribosomal RNA; NADH dehydrogenase subunit 7; H(+)-transporting ATPase subunit Subunits 1 and 2 of cytochrome c oxidase are expressed from a continuous open reading frame in the mitochondrial DNA of 1 (bases 1 to 41591)
Burger, G., Plante, I., Lonergan, K.M. and Gray, M.W.
The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba 24-AUG-1995 mitochondrial DNA. A case of evolutionary transfer of introns Predicted editing of additional transfer RNAs in Acanthamoeba cytochrome oxidase subunit 1; cytochrome oxidase subunit 2; ribosomal protein S4; Phe-tRNA; X-tRNA; NADH dehydrogenase subunit 5; NADH dehydrogenase subunit 1; cytochrome oxidase subunit 5; NADH dehydrogenase subunit 11; cytochrome oxidase subunit 2; ribosomal protein S2; His-tRNA; Leu-tRNA; H(+)-transporting ATPase subunit 9; Tyr-tRNA; cytochrome b; protein S11; ORFB; ORF25; Lonergan,K.M. and Gray,M.W. The ribosomal RNA gene region in Acanthamoeba castellanii NADH dehydrogenase subunit 3; NADH dehydrogenase subunit ACU12386 41591 bp DNA circular INV 24-AUG. Acanthamoeba castellanii mitochondrion, complete genome. castellanii. Complete sequence, gene content and genome !rp-tRNA; ribosomal protein L11; ribosomal protein S12; Eukaryotae; mitochondrial eukaryotes; Acanthamoebidae; ribosomal protein S19; ribosomal protein S3; ribosomal protein L16; ribosomal protein L14; NADH dehydrogenase subunit 4L; ORF83; ORF115; ribosomal protein 15; ribosomal protein 814; ribosomal protein 88; ribosomal protein 16; protein S7; ribosomal protein L2; castellanii mitochondria Nucleic Acids Res. 21 (18), 4402 (1993) Mitochondrion Acanthamoeba castellanii ORF349; Gln-tRNA; Lys-tRNA; Glu-tRNA. J. Mol. Biol. 239 (4), 476-499 (1994) between mitochondria and plastids? ribosomal protein S13; ribosomal Lonergan, K.M. and Gray, M.W. Lonergan, K.M. and Gray, M.W. Lonergan, K.M. and Gray, M.W. Acanthamoeba castellanii 3 (bases 5124 to 5757) (bases 5124 to 5757) 2 (bases 1 to 7352) 4 (bases 1 to 7352) Acanthamoeba. organization Unpublished Unpublished ribosomal 94275838 93157849 94021401 g562028 amoeba, 012386 4 DEFINITION ORGANISM REFERENCE AUTHORS JOURNAL JOURNAL ACCESSION REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL MEDLINE REFERENCE AUTHORS MEDLINE JOURNAL MEDLINE REFERENCE AUTHORS KEYWORDS TITLE TITLE TITLE TITLE SOURCE RESULT LOCUS

GenBank staff at the National Library of Medicine created this

DNA Cell Biol. 13 (11), 1127-1136 (1994)

95217333

JOURNAL MEDLINE REMARK

superoxide dismutase gene

(bases 1 to 12857)

AUTHORS

TITLE

REFERENCE

Unclassified. Homo sapiens

ORGANISM

Wan,X.S., Devalaraja,M.N. and St Clair,D.K. Molecular structure and organization of the human manganese

human embryoniclung fibroblast cell line WI38

q998582 577127

**ACCESSION** 

KEYWORDS

SOURCE

entry [NCBI gibbsq 164378] from the original journal article.

This sequence comes from Fig. 3.

Map location: 6. NCBI gi: 998582

/ ansigliue

POQAPRGLREQPERHRGEVPGGVGQGEMLQPR"

3748 t

3147 g

2627 c

3335

SASE COUNT

ORIGIN

Description: manganese superoxide dismutase/MnSOD"

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20; Mismatches 26; Indels 0; Gaps

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31; Conservative

Matches

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/note="human" 11351..11498)

mRNA

Location/Qualifiers

1..12857

source

FEATURES

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/product="Asp-tRNA"

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Gaps 1;

68 others

28-JUN-1994

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Gaps

1;

Score 138; DB 36; Length 1467; Pred. No. 2.58e+00; 26; Mismatches 42; Indels 1

Query Match 9.7%; Best Local Similarity 33.7%; Matches 35; Conservative

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Aug 27 18:29 BASE COUNT ORIGIN Church, S.L., Grant, J.W., Meese, E.U. and Trent, J.M.
Sublocalization of the gene encoding manganese superoxide dismutase (MnSOD/SOD2) to 6q25 by fluorescence in situ hybridization and Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Submitted (04-MAY-1992) to the EMBL/GenBank/DDBJ databases. S.L. Church, Washington Univ School of Medicine, Dept of Pediatric, 400 S Kingshighway Blvd, St Louis Children's Hospital, St Louis MO Eukaryotae; mitochondrial eukaryotes; Metàzoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; ö /clone lib="charon 21A"
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caagaga 648   :  : CARGARG 232		01-0CT-1991	es; d from ovis	•	7; 1; Gaps 1;	caagaga 648   :  : CARGARG 232		11-MAR-1993 n 9. cota group; tomia; Chordata; tygli; Chonata;	lutaminyl-tRNA
agatectt :   :NTGYCCN-	233 GNITYGAYCAYMGNGAYMSNAARGINWSNYINCARGARAARAY	TEPREPEL 1467 bp DNA BCT Leptospira hardjo repetitive element. M57713 g149621 repeat region. Leptospira hardjo DNA.	SM Leptospir Prokaryot Sprokaryot Sprokaryot Sprokaryot Nucleotid Laptospir L J. Gen. NGBI gi:	FEATURES Location/Qualifiers source 11467 /organism="Leptospira hardjo" /sequenced_mol="DNA" BASE COUNT 526 a 240 c 338 g 363 t	Query Match 9.7%; Score 138; DB 22; Length 1467; Best Local Similarity 33.7%; Pred. No. 2.58e+00; Matches 35; Conservative 26; Mismatches 42; Indels 1	Db 589 ggttgagtcattacaaatggttgaacaatcitcactttaacaacgagatccttcaagaga 648	Db 649 cgtttaacgattattatagtcgagtgagagttcaagaagaat 692   : : : : : :  :  :	RESULT 8 LOCUS HSGINRS09 267 bp DNA PRI- 11-MAR-1993 DEFINITION H.sapiens gene for glutaminyl-tRNA synthetase, exon 9. ACCESSION X72404 NID Q287775 Glutaminyl-tRNA synthetase. SOURCE human. ORGANISM Homo sapiens Eukaryotae, mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eukaryotae, mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eukaryotae, mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Carella (Source Colomata; Oreleichthyes; Sarcopteryglia, Choanata; Metazoa; Charlostomata; Oreleichthyes; Sarcopteryglia, Choanata; Metazoa; Charlostomata; Oreleichthyes; Sarcopteryglia, Choanata; Metazoa; Charlostomata; Charlostomata; Charlostomata; Metazoa; Charlosto	REFERENCE 1 (bases 1 to 267) AUTHORS Kaiser,E., Eberhard,D. and Knippers,R.  TITLE Exons encoding the highly conserved part of human glutaminyl-tRNA synthetase

# Aug 27 18:29 US-08:231-565A-2 rge

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Eukaryota; Animalia; Metazoa; Arthropoda; Uniramia; Insecta;
Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicoidea;
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1 (bases 1 to 1384)

Hoog, C., Dancholt, B. and Wieslander, L.

Terminal repeats in long repeat arrays are likely to reflect the early evolution of Balbiani ring genes
J. Mol. Biol. 200 (4), 655-664 (1988)
88316932
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                                                 Kunze, N., Bittler, E., Fett, R., Schray, B., Hameister, H., Wiedorn, K.H. and Knippers, R.
The human QARS locus: assignment of the human gene for glutaminyl-tRNA synthetase to chromosome 1q32-42 Hum. Genet. 85 (5), 527-530 (1990)
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J. Mol. Evol. 34 (1), 45-53 (1992)
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P SKHSKP SKHSKP SKHSKP SKHSKP EKCGSAMKR TEGEKCARKNGRFNSKRCTCTSAG **AEKGGKFDSATCKCTPEAVTEGPTTCLESSEDDDNIVCDDAMRKTESAKCAEKGGKFD** 

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CDS

source

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Galper, J.B. and Maas, R.L. Cloning and developmental expression of the chick type II and type

III TGF beta receptors Dev. Dyn. 199, 12-27 (1994)

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Location/Qualifiers

NCBI gi: 511842

94220749

MEDLINE JOURNAL

1..3347

source

FEATURES

COMMENT

/dev\_stage="embryonic"

/germline

Barnett, J.V., Moustakas, A., Lin, W., Wang, X.-F., Lin, H.L.,

Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.

transforming growth factor-beta receptor; transforming growth factor-beta type III receptor.

TGF-beta; betaglycan; plasma membrane;

g511842 mRNA,

KEYWORDS

ACCESSION

Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;

Gallus gallus

ORGANISM

SOURCE

Neognathae; Galliformes; Phasianidae.

(bases 1 to 3347)

AUTHORS REFERENCE

TITLE

Gallus gallus transforming growth factor-beta type III receptor

HRNA

3347 bp

CHKTGFBA

DEFINITION

12

RESULT

complete CDS.

20-JUL-1994

WRT

340 ccaacaacatgcattgaatccagtgaaagcgatgaagccacttcagctcctgaagtacca 399 

.. = = =

Gaps

17; Mismatches 26; Indels 1;

Length 1384;

Score 137; DB 28; Pred. No. 3.21e+00;

Query Match 9.6%; Best Local Similarity 41.3%;

31; Conservative

Matches

쉱 g g <u>ي</u>

357 t

293 g

245 c

489

BASE COUNT

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1349..1354

polyA signal

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2

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PSHMI AHQNWAPMQHQN ISHHFLGDLSGLDLQSSSGHAP IQTI LPQDSQRMAPPISST
QFLTPPSQHSYSNPMDNTPNHQQVPDHPFLTPSAGSPDQMSSSSPHSNLSDWSEGISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPCLP SPCRSGGTCVQTSDTTHTCSCLPGFTGQTCEHNVDDCTQHACENGGPCIDGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSCPRGTQGVHCEIDIDDCSPSVDPLTGEPRCFNGGRCVDRVGGYGCVCPAGFVGERC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HECQTRMDSPCLVNPCYNGGTCQPISDAPFYRCSCPANFNGLLCHILDYSFSGGQGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAL I FP YYGSEHELSKHKRSDWTDPGQLMQRARRSLTSFLKPRTRRELDHMEVKGS I V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSDVSSPPMMTSPFQQSPP ISINQIQGLADSHMGGALQGLGKPFDSAPRLSHLPVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HACMNSP CRNGGTCSLLTLDTFTCRCQP GWSGKTCQLADPCASNPCANGGQCSAFESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYNCHCDKHWTGQYCTEDVDECELSPNACQNGGTCHNTIGGFHCVCVNGWTGDDCSEN
IDDCASAACSHGATCHDRVASFFCECPHGRTGLLCHLDDACISNPCQKGSNCDTNPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKAICTCPPGYTGSACNQDIDECSLGANPCEHGGRCLNTKGSFQCKCLQGYEGPRCEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVNECKSNPCQNDATCLDQIGGFHCICMPGYEGVFCQINSDDCASQPCLNGKCIDKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFHCECPKGFSGSLCQVDVDECASTPCKNGAKCTDGPNKYTCECTPGFSGIHCELDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCPKGTTGVNCEINIDDCKRKPCDYGKCIDKINGYECVCEPGYSGSMCNINIDDCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPCHNGGTCIDGVNSFTCLCPDGFRDATCLSQHNECSSNPCIHGSCLDQINSYRCVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNQGSCIDDVAGFKCNCMLPYTGEVCENVLAPCSPRPCKNGGVCRESEDFQSFSCNCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNGGVCQDRVNGFVCVCLAGFRGERCAEDIDECVSAPCRNGGNCTDCVNSYTCSCPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIYCDVPSVSCEVAARQQGVSVAVLCRHAGQCVDAGNTHLCRCQAGYTGSYCQEQVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVASNTKHGYICKCQPGYSGSSCEYDSQSCGSLRCRNGATCVSGHLSPRCLCAPGFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMDGLDCADDVPQKLAVGSLVLVVHIPPDELRNRSSSFLRELSSLLHTNVVFRRDANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMF LVLLALAVLALAAVGVVVSRKRKREHGQLWF PEGFKVNEPKKKRREPVGEDSVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KP LKNSDSSLMDEQLSEWAEDDTNKRFRFEGQSI LEMSGQLDHRQWTQQHLDAADLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSMAPTPPQGQIENDCMDVNVRGPDGFTP1MIASCSGGGLENENGEAEEDPSADVITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIYHGANLHNQTDRTGETALHLAARYARSDAAKRLLESCADANVQDNMGRTPLHAAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ADAQGVFQILIRNRATDLDARMHDGTTPLILATRLAVEGMVEELINCHADPNAVDDSG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSA LHWAAAVNNVDAAVVI LKNGANKD LQNNKEETP LF LAAREGSYETAKVI LDHLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDIADHLDQLPRDIAHERMHHDIVRLLEEYNLVRSPPLPLSPPLCCPNTYLGIKPSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNNNTAKKTRKPGGKGVGGKDSGKDIRTKKKKSGDGKNGGIMEVGVLSPVDSLESPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRCPADFVGAQCQFPNPCNPSPCRNGGVCRPQMQGNEVGVKCDCVLGFSDRLCLTPVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ICTCPPNFHGQTCRQDVNECAVSPSPCRNGGTCINEVGSYLCRCPPEYTGPHCQRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGWMGRNCD IN INECLSNPCVNGGTCKDMTSGYLCTCRAGFSGPNCQMN INECASNPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A CWO GOT CEVD INECVRNPCTNGGVCENLRGGFOCR CNPGFTGALCEND IDD CEPNPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSGINCEINTPDCTESSCFNGGTCVDGISSFSCVCLPGFTGNYCQHDVNECDSRPCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGS CQDGYGTYKCTCPHGYTGLNCQSLVRWCDSSPCKNGGSCWQQGASFTCQCASGW]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAP PVEVEIRCEIAQCEGRGGNA I CDTQCNNHACGWDGGDCS LNFDDPWQNCSAALQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLEIDNRQCFQQSDECFQSATDVAAFLGALASSGNLNVPYIIEAVTSEGGPPKTGEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MNRFLVKLTLLTAASLATVAQGQRCSEYCQNGGICEYKPSGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECASSPCHYGVCRDGVASFTCDCRPGYTGRLCETNINECLSQPCRNGGTCQDRENAY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="transmembrane protein-precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="transmembrane protein"
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                                                                                                                                                                                                                                                                                    58..7471
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                                                                                                                                                sig_peptide
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                                                                                                                                                                                                                                                                                    CDS
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cosmid is ZC64, 200 bp overlap; 3' cosmid is T22B2. Actual start this cosmid is at base position 29748 of CELZC64. ပ Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Deer, S., Du, Z., Durbin, R., Favello, A., Fluton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jonnes, M., Kershaw, J., Kirsten, J., Laster, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., Ξ 2.2 Mb of contiguous nucleotide sequence from chromosome III of Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., 2646 cttgttctccacgtccctgtaaaaacggcggtgtgtgtcgtgaatctgaggatttccaga 2705 2706 gcttctcctgtaactgtccggctggatggcaa-ggtcaaacgtgtgaggtggacattaat 2764 e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk 274 TYTTYTCYTGNARNWSNACYTTNWSRTCNCKRTGRTGRARNCCYTCYTGNGGRCANCKNC 215 334 SYTGYTCNGCNWSNARYTTYTCRTANGCNGGNGGNGCRTTNGGNACNACNGGYTCRCART 275 214 KNGTNARNGCRCAYTGNGTNCCNACRTGNARNWSYTTRTCCATNARNGCNCKRTANCCRT 155 Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., 25-NOV-1995 Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Gaps O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., gagtgtgtgaggaacccgtgcactaatggaggagtgtgtgaaaacctgcgcggtggattt Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; <u>:</u> Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Indels ΙΝ NEIGHBORING COSMID INFORMATION: 36; Mismatches 97; Caenorhabditis elegans strain=Bristol N2. Direct Submission Submitted (16-NOV-1995) Robert Waterston Cambridge CB10 IRO, England the sequence of C. elegans cosmid F47F2 Sanger Centre, Hinxton Hall <u>::</u> Genome Sequencing Center Caenorhabditis elegans cosmid F47F2. Wilkinson-Sproat, J. and Wohldman, P. Nature 368 (6466), 32-38 (1994) Rhabditidae; Caenorhabditis. DNA Submitted by: Caenorhabditis elegans (bases 1 to 24537) 24537 bp (bases 1 to 24537) (bases 1 to 24537) Conservative 2825 cagtgccgctgcaat 2839 154 TNCKNCKNCKRCART 140 Unpublished (1995) :: Waterston, R. Bentley, D. CELF47F2 g1072202 94150718 elegans 040943 61; DEFINITION ORGANISM JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT REFERENCE AUTHORS 2765 Matches REFERENCE AUTHORS JOURNAL MEDLINE ACCESSION KEYWORDS TITLE RESULT SOURCE LOCUS QIN 셤 g, 음 გ g ဥ 쇰 გ

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519 q467672 repeat\_region X77623 13 source DEFINITION ORGANISM BASE COUNT Matches JOURNAL JOURNAL REFERENCE AUTHORS ACCESSION REFERENCE AUTHORS KEYWORDS SOS FEATURES TITLE COMMENT ORIGIN SOURCE LOCUS 원 à à SMARFYASEIVCALEYIHSIGIVYRDIKPENIMLSKEGHIKMADFGFAKELRDRTYTI CGTPDYLAPESIARTGHNKGVDWMALGILIYEMMVGKPPFRGKTTSEIYDAIIEHKIK FPRSFNIAAKDIVKKLLEVDRTQRIGCMKNGTQDVKDHKWFEKVNWDDTLHIRVEPPI VPTLYHPGDTGNFDDYEEDTTGGPLCSQRDRDLFAEW" /translation="MADPLFYGGDAAAHMSFSSGGGGCDEAVRNNDARAAFNLHIN THWKLSITPTRESFSLSQLERIITIGKGTFGRVELARDKITGAHYALKVLAITGRVDM RQTQHVHNEKRVLLQLKHPFIVKMYASEKDSNHLYMIMEFVPGGEMFSYLRASRSFSN /translation="MYPNPAFGSPRNPGSTGSSRGMSMNRYPFVNRNPAVRTTTAAPK LLTPKKQCANACMPQCTPRCLQRYNQIVASFMNSLTAIDVMGQPVNEEPRKSIRFSPK KGI ECRDECMPYCTPQCLDAYSIAEHNAKPKVCKAVCMPDCTEECITAPPLMVPCIFD NVCHCPAGYVRCSEMTCCMKYKTMAVRYKNKMTSMSFSDDDEKYSKDSGNETSVYMSE /translation="MSSSTSSVESVEDESCSNECSASFTFDTNNNSRGNNQVNELAEE Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier,  ${\tt ms}$  in preparation) /note="similar to the catalytic subunit of cAMP-dependent protein kinase; NCBI gi: 1072204" join(11794..11910,11960..12050,14384..14552,14611..14700, 14794..14872,14923..15017,15774..15989,16039..16174, <u>;</u> complement (join (17302..17414,17513..17567,17620..17734, 17780..17870,18097..18223,18276..18362,18787..18984)) 3043 ttcacacatttcttctcgaaatacctccttatcagtctcagtgatcgttcccctccagag 3102 Gaps 18; Mismatches 17; Indels 1; Score 137; DB 28; Length 24537; Pred. No. 3.21e+00; LRNMGGGSIVYYPEQGKAEILKNDGSVVVEVMESAQETNFEDN /organism="Caenorhabditis elegans" complement(join(8747..8859,10794..10866)) 4106 g 8363 t /evidence=not\_experimental /gene="F47F2.1" /evidence=not\_experimental /gene="F47F2.3" /evidence=not\_experimental /gene="F47F2.2" /note="NCBI gi: 1072205" /note="NCBI gi: 1072203" /db xref="PID:g1072205" 'db\_xref="PID:g1072203" 'db\_xref="PID:g1072204" NCBI gi: 1072202 Location/Qualifiers PQYMYTGTYLARAVGEQ" /codon start=1 codon start=1 codon start=] 16225..16347) 9.6%; 4329 c 27; Conservative /map="X" /map="X" 1..24537 "X"=dem/ Best Local Similarity 7739 3103 aac 3105 NOTES: Query Match source BASE COUNT Matches S FEATURES CDS CDS ORIGIN

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Pacciarini, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia, Via Bianchi, 7, 25125 Brescia, ITALY NCBI gi: 467672 IKKLKTEWNEIHCCYEAGVTGYPLYRYLKSLGVNCILVAPGKIPROSSDKIKTDKRDA IKLARLMRSGELES I HVPSEEDEAVRDYLRSRDSLRLDLGRNRQRLMKFLLRKD IKYS TTKYWTVSHYKWINNLHFNNEILQETFNDYYSRVRVQEENLKAMDKKIQEIAESEPYR /translation="MKRKVYVGMDVHKETIQIAYLTSNSKEILKEQQIKHNEVQIKKF EKVGILRCFRGVDYLTAMFLLCEVNDFKRFKTAGSFMSFLGLVPGEYSSGSKRKQTGI TKTGSPRLRRILTEAAWQHRFPGTGSKIVTARRSGQPALVVALAEKASLRLHKKFRNI Herbaspirillum seropedicae nifA (NifA) gene complete CDS, and nifB (NifB) gene 5' end. Submitted (03-FEB-1994) to the EMBL/GenBank/DDBJ databases. M.L. 593 agtcattacaaatggttgaacaatcttcactttaacaacgagatccttcaagagacgttt 652 19-AUG-1991 Gaps 22-MAR-1994 Eubacteria, Spirochaetales, Leptospiraceae, Leptospira. 1 (bases 1 to 1458) 25; Mismatches 40; Indels 1; Length 1458; /organism="Leptospira borgpetersenii" BCT BCT /insertion\_seq="IS-like element" 653 aacgattattatagtcgagtgagagttcaagaagagaat 691 Score 133; DB 22; Pred. No. 7.52e+00; QLRGKTPQVMITAVSRELSGFLWAAMNLVA" /clone\_lib="plasmid; pUC8" /clone="pT10, pT126" /note="serovar tarassovi" group(12..19,1445..1452) /note="IS-like element" /note="NCBI gi: 467673" /strain="Mitis-Johnson' /product="transposase" /db xref="PID:g467673" insertion element; transposase. 332 g L.borgpetersenii IS-like DNA Location/Qualifiers /rpt\_type=INVERTED 92..1186 Leptospira borgpetersenii. Leptospira borgpetersenii table=11 codon start= 3287 bp Query Match 9.4%; Best Local Similarity 33.3%; (bases 1 to 1458) 33; Conservative Direct Submission 1..1458 /trans] Pacciarini, M.L. Pacciarini, M.L. Unpublished HEUNIFABX 14 RESULT

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//translation="MATILDDRSVNLELVTIYEISKILGSSLDLSKTLREVLAVLSAH
//translation="MATILDDRSVNLELVTIYEISKILGSSLDLSKTLREVLAVLSAH
GEFURKVLLSLAGDSGELQLYSRAIGSYEERQSRYRROGGSTRKREGEFPIVYRRLA
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QSAPSRSTMLLRGESGTGKEVIARAIHYLSPRKDGPFIKVNCAALSETLLESELFGHE
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Padmadevwekvknhpcyseeahhhyarmhvavapacniocnycnrkydcanesrpcy
VSEKLTPEQAAKKVFAVASTIPOMTVLGIACPGDPLANPAKTFKTFELISQTAPDIKL
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                                                                                                                   Prokaryotae; Gracilicutes; Scotobacteria; Aerobic/microaerophilic, motile, helical/vibrioid bacteria.
                                                                                                                                                               Souza, E.M., Funayama, S., Rigo, L.U., Yates, M.G. and Pedrosa, F.O. Sequence and structural organization of a nifA-like gene and part of a nifB-like gene of Herbaspirillum seropedicae strain 278 J. Gen. Microbiol. 137, 1511-1522 (1991)
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                         elongation growth factor receptor-related; nifA gene; nifB gene;
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                                                  oncogene; transmembrane protein; tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                'organism="Herbaspirillum seropedicae"
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                                                                        Herbaspirillum seropedicae (strain 278) DNA.
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Pred. No. 7.52e+00;
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15-FEB-1993

LOCUS OATCVG6 708 bp RNA MI DEFINITION O.aries rearranged T-cell receptor gamma.

RESULT

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/translation="MGFSLGAEGRAVLGRLALLWALVVPGIQQEIRLSQRSVMVGSAG
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                                                                                  Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                             and developmentally regulated expression of the sheep gamma/delta
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                                                                                                                                                                                                                                                                                             R. Hein, Basel Institute for Immunology, Grenzacherstrasse, 487, CH-4058 Basel, Switzerland
2 (bases 1 to 708)
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                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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I-cell receptor; I-cell receptor gamma chain.
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Pred. No. 9.28e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="61 day old
/cell_type="peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Ovis aries"
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NCBI gi: 2278
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Best Local Similarity 37.8%;
Matches 28; Conservative
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148..>708
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                                                                                                                                                                                                                                               Direct Submission
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Tue Aug 27 08:08:49 1996; MasPar time 3.69 Seconds 282.669 Million cell updates/sec Run on:

Tabular output not generated.

(1-118) from US08231565A.pep 889 >US-08-231-565A-2 Description: Title:

1 MPREDAHFIYGYPKKGHGHS.........NAPPAYEKLSAEQSPPPYSP 118 Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

76839 seqs, 8833555 residues Searched:

Minimum Match 08 Listing first 45 summaries Post-processing:

a-geneseq23

Database:

Mean 29.335; Variance 113.395; scale 0.259 Statistics:

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

No. Score Match Length DB   ID   Description   Pred. No.	•													
Query Score Match Length DB ID  889 100.0 118 15 R84212 889 100.0 118 11 R63158 90 10.1 380 1 R63290 83 9.3 200 15 R82900 83 9.3 306 12 R82900 82 9.2 897 4 R20982 81 9.1 855 10 R51248 81 9.1 855 10 R51248		Pred, No.	1.71e-83	1.71e-83		_	_			1.65e+01	1.98e + 01	_	_	_
Autor Match Length DB 889 100.0 118 15 889 100.0 118 11 90 10.1 18 11 90 10.1 18 11 90 10.1 18 11 90 10.1 18 11 90 10.1 18 11 90 10.1 18 11 90.1 855 10 81 9.1 855 10 81 9.1 855 10		Description	MART-1 melanoma antig	Tumour rejection anti	cPA-P2 Hybrid plasmin	Mouse B7-1 (IqV-like	Mouse B7-1 IgV-like i	Mouse B7-1 alternativ	Murine B lymphocyte a	Sequence of beta-chai	Hepatocyte nuclear fa	FIV UK2 envelope prot	FIV petaluma envelope	FIV PET-F14 envelope
Score 889 90 90 90 83 83 83 83 81 81 81 81		ΩI	R84212	R63158	_R05433	R82900	R82902	R82893	R67990	R20982	R28757	R51252	R51248	R51249
Score 889 90 90 90 83 83 83 83 81 81 81 81		88	15	11	-	15	15	15	12	7	S	10	10	10
Score 889 90 90 90 83 83 83 83 81 81 81 81		Length	118	118	380	200	212	306	306	897	455	855	928	856
Sc	o\o	Query Match	100.0	100.0	10.1	9.3	9.3	9.3	9.3	9.5	9.1	9.1	9.1	9.1
Result No. 1 1 2 2 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4		Score	88	88	90	83	83	83	83	85	81	81	81	81
		Result No.	1	2	m	4	5	9	7	<b>0</b> 0	6	10	11	12

Aug 27 (	07:56				US-08-23	US-08-231-565A-2 rag	
13	81	9.1	856	2	R51247	FIV envelope protein	1.98e+01
14	79	8.9	234	က	R13844	Fusaric acid resistan	2.84e+01
15	79	8.0	854	10	R51250	FIV PPR envelope prot	2.84e+01
16	79	8.9	856	10	R51254	FIV DUTCH19K1 envelop	2.84e+01
17	79	8.9	940	7	R07070	Fibronectin-binding p	2.84e+01
18	9/	8.5	524	7	R05077	Sall restriction prod	4.86e+01
19	9/	8.5	524	-	P90113	Rabies G protein	
20	9/	8.5	854	œ	R44957	Feline Immunodeficien	4.86e+01
21	9/	8.5	1822	10	R55273	Beta subunit of integ	4.86e+01
22	75	8.4	117	7	R07997	Human CD2 cytoplasmic	5.80e+01
23	75	8.4	332	13	R74221	Epitope on the primar	5,80e+01
24	75	8.4	345	15	R77026	Canine herpesvirus gD	5.80e+01
25	75	8.4	351	4	R20803	Human CD2 antigen.	5.80e+01
56	75	8.4	351	7	R11921	Human T11 sugar prote	5.80e+01
27	75	8.4	353	7	R06365	Soluble two domain hu	5,80e+01
28	75	8.4	360	-	P81178	Sequence of human Tll	5.80e+01
29	75	8.4	855	10	R58585	FIV UK8 envelope prot	5.80e+01
30	75	8.4	822	10	R51255	2 envelor	5.80e+01
31	75	8.4	870	6	R51246	Composite sequence of	5.80e+01
32	74	8.3	132	7	R36393	Penetrin.	6.91e+01
33	74	8	577	-	R04924	Immunoprotein TANG12.	6.91e+01
34	74	8.3	1026	Ξ	R58906	Human protocadherin-4	6.91e+01
35	74	8.3	1203		R58911	Product of alternativ	6.91e+01
36	73	8.3	10	15	R84778	MART-1 melanoma antig	8.23e+01
37	73	8.2	238	7	P70375	Human interleukin-2 r	8.23e+01
38	73	8.5	272	c	P50001	Sequence of interleuk	8.23e+01
39	73	8.2	272	14	R79389	Human interleukin-2 r	8.23e+01
40	73	8.2	272	ო	P61052	Sequence encoding int	8.23e+01
41	73	8.2	968	4	R21580	Plasma membrane proto	8.23e+01
42	72	8.1	10	15	R84777	MART-1 melanoma antig	9.80e+01
43	72	8.1	479	-	P81013	Complete sequence of	9.80e+01
44	72	8.1	479	m	P50034	Sequence encoded by t	9.80e+01
45	72	œ 	1091	7	P98500	Partial sequence enco	9.80e+01

### ALIGNMENTS

in insect cell cultures. MART-1 protein is a source of immunogenic peptides (see R84196 for peptide M9-2) which are optionally modified (see R84783-R84800) and used in medicaments for the treatment or

prevention (by immunization) of melanoma. Antibodies against MART-1 and its immunogenic peptides may be used in the detection and

88888888

isolation of MART-1 from a sample, the detection of which is indicative of a disease state (melanoma or metastatic melanoma)

m

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Gaps

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0; Indels

Pred. No. 1.71e-83; Score 889; DB 15; 0; Mismatches

Best Local Similarity 100.0%;

Query Match

118; Conservative

Matches

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ð g à

100.0%;

118 AA;

Sequence

Length 118;

9

1 mpredahfiygypkkghghsyttaeeaagigiltvilgvllligcwycrrrngyralmdk

slhvgtqcaltrrcpqegfdhrdskvslqekncepvvpnappayeklsaeqspppysp 118 61 SLHVGTQCALTRRCPQEGFDHRDSKVSLQEKNCEPVVPNAPAXEKLSAEQSPPPYSP 118

5

Tumour rejection antigen; precursor; HLA-A2 molecule; tyrosinase;

Tumour rejection antigen precursor.

(first entry)

26-MAY-1995

R63158 standard; Protein; 118 AA.

RESULT

isolation; melanoma; cell line; LB-39-MEL; diagnosis; vaccine;

urokinase linker, and an urokinase protease domain wherin glycine residue The compound is used to treat thromboembolic disease esp. with myocardial Gene encodes hybrid plasminogen activator (PA) comprising Kringle 1, an infarction, has a longer half-life than free PA and targets the heparin Compsn. contg. plasminogen activator conjugated to heparin component used for treatment of thromboembolic disease, with longer half 7 lalllllllpgcwasecktgdgknyrgtmsktkn-gitcgkwsstsphrprfspathps 65 Gaps Mouse B7-1 (IgV-like domain deleted). T-cell costimulatory molecule; B7-1; T-lymphocyte; CD28; CTLA4; .. 8 site of thrombus or embolism reducing the risk of reocclusion. 15; Mismatches 24; Indels Plasminogen activator; fibrin; urokinase; thromboembolic Score 90; DB 1; Length 380; Location/Qualifiers R82900 standard; Protein; 200 AA. 07-MAY-1996 (first entry) receptor; immunoglobulin. 169..200 Peptide 1..37 /label= Sig\_peptide Domain 169.. 66 egleenyc 73 86 VSLQEKNC 93 Mus musculus. R82900; RESULT 쇰 ð g ð THE ENDING THE STATE OF THE STA

;

This sequence represents the tumour rejection antigen precursor which is

used for developing prods. for diagnosis or treatment of expression

related disorders, partic. melanoma Claim 5; Page 14; 26pp; English.

Nucleic acid coding for a tumour rejection antigen precursor - is

Traversari C;

Brichard V, De Plaen E,

(LUDW-) LUDWIG INST CANCER RES.

Van Pel A, Wolfel T;

WPI; 94-316544/39. Boon-Falleur T,

N-PSDB; 076370.

18-MAR-1993; US-032978.

09-MAR-1994; U02487

29-SEP-1994

Homo sapiens. WO9421126-A.

therapy.

LB-39-MEL. The tumour rejection antigen may be used for diagnosis or in vaccines or for therapy of disorders characterised by the expression processed to a tumour rejection antigen presented by HIA-A2 molecules. The tumour rejection antigen is not related to tyrosinase. The cDNA encoding this sequence was isolated from the melanoma cell line,

of the tumour rejection antigen precursor, particularly melanoma

Sequence

0; Indels 0; Gaps 0;

100.0%; Score 889; DB 11; Length 118; 100.0%; Pred. No. 1.71e-83;

Best Local Similarity 100.0%;

Query Match

118; Conservative

Matches

g 8 셤 δ

0; Mismatches

8

1 mpredahfiygypkkghghsyttaeeaagigiltvilgvllligcwycrrrngyralmdk 60

1 MPREDAHFIYGYPKKGHGHSYTTAEEAAGIGILTVILGVLLLIGCWYCRRNGYRALMDK

/label= Cytoplasmic\_domain /note= "cytoplasmic\_domain is encoded by exon of the B7-1 gene" W09523859-A2.

S

212 AA;

158 gagfgavitvvvivviikc-fckhrscfr 185 Best Local Similarity 27.6%; 8; Conservative Matches g

R82893 standard; Protein; 306 AA.

R82893;

T-cell costimulatory molecule; B7-1; T-lymphocyte; CD28; CTLA4; Mouse B7-1 alternatively spliced form.

Location/Qualifiers Peptide

/label= Sig\_peptide WO9523859-AZ. 08-SEP-1995

1;

Gaps

6; Indels 1;

14; Mismatches

146 gagfgavitvvvivviikc-fckhrscfr 173 :||:| : ::::| | :|::|: :|
27 AAGIGILTVILGVLLIGCWYCRRNGYR 55

셤 δ

9.3%; Score 83; DB 15; Length 200; 7.6%; Pred. No. 1.37e+01;

Best Local Similarity 27.6%;

Sequence Query Match 8; Conservative

Matches

Sharpe AH;

Borriello F, Freeman GJ, Nadler LM, WPI, 95-320574/41.

Novel T cell co-stimulatory molecules - corresponding to naturally occurring alternatively spliced forms of T cells co-stimulatory

Disclosure; Page 49-51; 111pp; English. An alternatively spliced form of murine T-cell costimulatory

molecule B7-1 (R82893) is encoded by exons 1-6 (T01040) of the B1-7 gene. It includes cytoplasmic domains (R82887 and R82888) encoded by exons 5 (T01035) and 6 (T01034). Novel cytoplasmic forms of T-cell costimulatory molecules have been produced that bind to 

Sequence

Gaps ä 9.3%; Score 83; DB 15; Length 306; 7.6%; Pred. No. 1.37e+01; 6; Indels 14; Mismatches Best Local Similarity 27.6%; 8; Conservative Query Match Matches

1;

:||:| : ::::| | :|::|::|
27 AAGIGILTVILGVLLLIGCWYCRRNGYR 55 염 ð

R67990 standard; Protein; 306 AA. R67990; 

Murine B lymphocyte antigen B7 (mB7). 21-AUG-1995 (first entry)

B lymphocyte activation antigen; B7-1; Ig superfamily; CD28;

Aug 27 07:56

transmembrane domain, i.e. the IgC-like domain is deleted. encoded by exons 1, 2, 4 and 5 of the B7-1 (T01049) gene. This IgV-like isoform of B701 was expressed in CHO cells.

triggered a costimulatory signal in T-cells, causing stimulation of interleukin-2 prodn.

Sequence

Gaps 1 Score 83; DB 15; Length 212; Pred. No. 1.37e+01; 6; Indels 14; Mismatches 9.38; Query Match

;

:||:| : :: ::::| | :|::|:::|
27 AAGIGILTVILGVLLLIGCWYCRRNGYR 55

ð

07-MAY-1996 (first entry)

Disclosure; Page 55-56; Illpp; English.
A naturally occurring form of mouse T-cell costimulatory molecule B7-1 (R82900) has the signal peptide directly linked to the IgC-like domain, i.e. the IgV-like domain is deleted. It is encoded by exons 1, 3, 4 and 5 (see T01047) of the B7-1 gene. An alternatively spliced form of IgV-deleted B7-1 (R8291) is encoded by exons 1, 3, 4 and 6. T-cell costimulatory molecules can be produced in which the IgV-like domain is deleted.

Novel T cell co-stimulatory molecules - corresponding to naturally

Sharpe AH;

Borriello F, Freeman GJ, Nadler LM,

WPI; 95-320574/41.

N-PSDB; T01047.

(BGHM ) BRIGHAM & WOMENS HOSPITAL. (DAND ) DANA FARBER CANCER INST.

02-MAR-1995; U02576. 02-MAR-1994; US-205697.

08-SEP-1995.

occurring alternatively spliced forms of T cells co-stimulatory

molecules or variants

receptor; immunoglobulin.

Mus musculus

02-MAR-1995; U02576. 02-MAR-1994; US-205697.

(BGHM ) BRIGHAM & WOMENS HOSPITAL. (DAND ) DANA FARBER CANCER INST.

molecules or variants

T-cell costimulatory molecule; B7-1; T-lymphocyte; CD28; CTLA4;

Mouse B7-1 IgV-like isoform.

07-MAY-1996 (first entry)

R82902;

R82902 standard; Protein; 212 AA.

receptor; immunoglobulin; interleukin-2,

Mus musculus.

Location/Qualifiers

1..37

Peptide Domain /note= "cytoplasmic domain is encoded by exon 5 of the  $B7-1\ gene"$ 

WO9523859-A2 08-SEP-1995.

/label= Cytoplasmic domain

181..212

/label= Sig\_peptide

CD28 or CTLA4 and trigger a costimulatory signal in T-cells. 306 AA;

252 gagfgavitvvvivviikc-fckhrscfr. 279

RESULT

Novel T cell co-stimulatory molecules - corresponding to naturally

Sharpe AH;

02-MAR-1995; U02576. 02-MAR-1994; US-205697. (BGHM ) BRIGHAM & WOMENS HOSPITAL. (DAND ) DANA FARBER CANCER INST. Borriello F, Freeman GJ, Nadler LM,

WPI; 95-320574/41.

N-PSDB; T01049

occurring alternatively spliced forms of T cells co-stimulatory

A naturally occurring form of mouse T-cell costimulatory molecule B7-1 (R82902) has the IgV-like domain directly linked to the

Disclosure; Page 91-92; 111pp; English.

molecules or variants

transmembrane protein.

; Gaps It can be found in Genbank at Accession no. X60958. The encoded protein, R67990, binds both human CTLA4 and human CD28. It is related to human hB7-2 (see Q81351) and human hB7-1 (see Q81371). Part of R67990 (see CC) is published in Freeman, G.J. et al. J. of Experimental Medicine, in press at the time when the patent Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful Ξ for enhancing or suppressing T-cell mediated immune responses lymphocytes, cell lines 702 and A20, clones B7 nos. 1 and 29 diagnosis; granulocyte-macrophage colony stimulating factor. Agonist; antagonist; myeloid leukaemia; therapy; screening; 9.3%; Score 83; DB 12; Length 306; Disclosure, pages 118-120, 175pp; English. 081371 is in pCDM8 vector. It is derived from germline B 6; Indels Sequence of beta-chain of a human granulocyte-macrophage colony stimulating factor (GM-CSF) receptor. Freeman GJ, Gray GS, Greenfield E, Nadler IM; Pred. No. 1.37e+01; 14; Mismatches 252 gagfgavitvvvivviikc-fckhrscfr 279 :||:|: :: ::::| | :|::||: :|
27 AAGIGILTVILGVLLIGCWYCRRRNGYR 55 /label= Ig c-set domain Misc\_difference 1..306 /label= published /note= "Freeman, G.J. et al. see CC" (DAND ) DANA FARBER CANCER INST INC. Location/Qualifiers 1..17 /label= transmembrane 273..306 /label= intracellular (cytoplasmic) Location/Qualifiers R20982 standard; Protein; 897 AA. Best Local Similarity 27.6%; 8; Conservative 17-MAY-1992 (first entry) 248..272 143..236 application was written. Sequence 306 AA; 38..142 /label= signal sequence
/note= "hydrophobic" 38..247 'label= Ig V-set domain 26-JUL-1993; US-101624. 19-AUG-1993; US-109393. 03-NOV-1993; US-147773 /label≈ extracellular (REPK ) REPLIGEN CORP. 26-JUL-1994; U08423. WPI; 95-075236/10. N-PSDB; 081372. /label= signal Aus musculus. Homo sapiens. 02-FEB-1995. WO9503408-A. /note= "6" Query Match Protein Peptide R20982; Domain Domain Jomain Domain Matches 쇰 à ID DE DE OS OS ETT ETT

US-08-231-565A-2.rag Aug 27 07:56

**.**--

Modified -site 58..60

Gaps contains a region with two potential zinc fingers between amino acids 50 and 116, which is 40 to 63% identical to the zinc finger (DNA binding) domain of other members of the steroid receptor superfamily. The proposed regulatory protein for mouse MHC I (HZ-RIIBP) had the greatest similarity (62.7%), with human thyroid hormone receptor (c-erbA, 73-78) having 59.7% identity in this This sequence was deduced from the cDNA sequence. The protein has The nucleic acid encoding the human GM-CSF beta-chain is isolated for screening agonists and antagonists of human GM-CSF, e.g. for from a cDNA library prepd, from poly (A) + RNA from TF-1 cells. Thigh affinity human GM-CSF receptor (Kd < 1 nM) can be used for screening candidate GM-CSF agonists and antagonists e.g. for Hepatocyte nuclear factor 4. (HNF4) hepatocyte nuclear factor 4; apolipoproteins; fat; cholesterol; Apo CIII; Apo Al; Apo B; pyruvate kinase; alpha l antitrypsin; glutamine synthetase; coronary heart disease hyperlipidaemia; Beta-chain of human granulocyte-macrophage CSF receptor - used a structure analogous to that of steroid/hormone receptors. It 4; antibodies - useful for treating cardiovascular diseases e.g. Score 82; DB 4; Length 897; Pred. No. 1.65e+01; 14; Mismatches 10; Indels Hepatocyte nuclear factor 4 and its DNA, regulation and 528 gfgdsevspltiedpkhvcdppsgpdttpaasdlptegppsp 569 atherosclerotic heart disease, hyperlipidaemia and liver disease; arteriosclerosis; obesity; ss. arteriosclerosis; also as an anorectic Hayashida K, Kitamura T, Miyajima A; WPI; 92-064947/08. Claim 2; Page 15-18; 26pp; English. Disclosure; Fig 3; 100pp; English. R28757 standard; Protein; 455 AA. (UYRQ ) UNIV ROCKEFELLER.
Darnell JE, Sladek FM, Zhong W;
WPI; 92-250081/30.
N-PSDB; Q31765. diagnosing myeloid leukaemia reating myeloid leukaemias. Query Match 9.2%; Best Local Similarity 33.3%; 14-JAN-1993 (first entry) 14; Conservative /label= glycosylation Modified -site 191..193 Modified -site 346..348 18-JUL-1990; US-554745. 23-DEC-1991; U09733. 21-DEC-1990; US-631720. (SCHE ) SCHERING CORP. 06-FEB-1992. 16-JUL-1991; U04846. /label= as above /label= as above N-PSDB; Q21453 W09211365-A. W09201788-A. 09-JUL-1992 Sequence Matches 염 δ

4;

0

feline immunodeficiency infection

# US-08-231-565A-2 rag

Disclosure; Figure 2; 68pp; English.

ö strains and serotypes. The consensus sequence basedon these, is given in R51247. The synthetic FIV peptides of the invention were derived principally from a combination of the sequences of the FIV UK 8 and Petaluma isolates, a composite sequence of which is given in R51246. feline immunodeficiency virus (FIV) envelope protein from different strains and serotypes. The consensus sequence basedon these, is given in R51247. The synthetic FIV peptides of the invention were derived serotypes, isolates of different geographical origin or even between Petaluma isolates, a composite sequence of which is given in R51246. Gaps principally from a combination of the sequences of the FIV UK 8 and Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS; T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein. feline immunodeficiency virus (FIV) envelope protein from different Variations in the sequence may occur between different strains or Variations in the sequence may occur between different strains or The sequences given in R51248-R51262 and R58584-85 represent the nucleic acid - used to prepare prods. for combating or diagnosis Disclosure; Figure 2; 68pp; English. The sequences given in R51248-R51262 and R58584-85 represent the .; 0 Score 81; DB 10; Length 855; Pred. No. 1.98e+01; 1; Mismatches 3; Indels Feline immunodeficiency virus antigenic polypeptide(s) and FIV petaluma envelope protein sequence. different isolates from the same host. of feline immunodeficiency infection Peptide 1..178 /note= "Hydrophobic leader peptide" Region 51..66 Location/Qualifiers R51248 standard; peptide; 856 AA. /note= "Transmembrane protein" /note= "Surface glycoprotein" 9.1%; 08-OCT-1994 (first entry) 11; Conservative 789 gilgiglgvlllilc 803 179..610 451..483 (PITM ) PITMAN MOORE INC. 360..424 539..567 31 GILTVILGVLLLIGC 45 95..173 21-SEP-1992; GB-019936. 20-SEP-1993; G01974. Best Local Similarity 855 AA; WPI; 94-118168/14. /note= "V1 region" 'note= "V2 region" /note= "V3 region" /note= "V4 region" /note= "V5 region" 31-MAR-1994. W09406471-A Synthetic. Francis MJ Sequence Query Match Protein Protein Peptide R51248; Region Region Region Region Region Matches 

790 gilgiglgvlllilc 804

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31 GILTVILGVLLIGC 45

ö ö of feline immunodeficiency infection
Disclosure; Figure 2; 68pp; English.
The sequences given in R51248-R51262 and R58584-85 represent the
feline immunodeficiency virus (FIV) envelope protein from different
strains and serotypes. The consensus sequence basedon these, is given
in R51247. The synthetic FIV peptides of the invention were derived
principally from a combination of the sequences of the FIV UK 8 and serotypes, isolates of different geographical origin or even between serotypes, isolates of different geographical origin or even between different isolates from the same host. Gaps Gaps FIV PET-F14 envelope protein sequence. Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS; T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein. etaluma isolates, a composite sequence of which is given in R51246. Variations in the sequence may occur between different strains or Feline immunodeficiency virus antigenic polypeptide(s) and nucleic acid - used to prepare prods. for combating or diagnosis ö ö Query Match 9.1%; Score 81; DB 10; Length 856; Best Local Similarity 73.3%; Pred. No. 1.98e+01; Score 81; DB 10; Length 856; Pred. No. 1.98e+01; 3; Indels 3; Indels Mismatches Mismatches different isolates from the same host. Location/Qualifiers /note= "Hydrophobic leader peptide" R51249 standard; peptide; 856 AA. /note= "Transmembrane protein" Protein 1/7...../note= "Surface glycoprotein" - :-- 360..424 Query Match 9.1%; Best Local Similarity 73.3%; 11; Conservative 08-OCT-1994 (first entry) 11; Conservative 451..483 611..856 (PITM ) PITMAN MOORE INC. 790 gilgiglgvlllilc 804 539..567 31 GILTVILGVLLIGC 45 51..66 95..173 20-SEP-1993; G01974. 21-SEP-1992; GB-019936. 1..178 /note= "V3 region" /note= "V4 region" /note= "V5 region" /note= "Vl region" /note= "V2 region" WPI; 94-118168/14. 409406471-A. 31-MAR-1994. Francis MJ; Synthetic. Sequence Sequence Protein Peptide Region Region Region legion Matches Matches 9 8 8 8 ð 

ö feline immunodéficiency virus (FIV) envelope protein from different strains and serotypes. The consensus sequence basedon these, is given in R51247. The synthetic FIV peptides of the invention were derived principally from a combination of the sequences of the FIV UK 8 and Petaluma isolates, a composite sequence of which is given in R51246. Variations in the sequence may occur between different strains or serotypes, isolates of different geographical origin or even between different isolates from the same host. Gaps Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS; T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein. nucleic acid - used to prepare prods. for combating or diagnosis Disclosure; Figure 2; 68pp; English. The sequences given in R51248-R51262 and R58584-85 represent the 0 Feline immunodeficiency virus antigenic polypeptide(s) and Score 81; DB 10; Length 856; Pred. No. 1.98e+01; 3; Indels US-08-231-565A-2.rag 1; Mismatches FIV envelope protein consensus sequence. of feline immunodeficiency infection Location/Qualifiers Peptide 1..178 /note= "Hydrophobic leader peptide" R51247 standard; peptide; 856 AA. /note= "Transmembrane protein" WO9406471-A. /note= "Surface glycoprotein" Region 360..424 Query Match 9.1%; Best Local Similarity 73.3%; 08-0CT-1994 (first entry) 11; Conservative (PITM ) PITMAN MOORE INC. 179..610 451..483 539..567 611..856 790 gilgiglgvlllilc 804 31 GILTVILGVLLLIGC 45 95..173 1..66 20-SEP-1993; G01974. 21-SEP-1992; GB-019936. /note= "V3 region" WPI; 94-118168/14. /note= "V1 region" /note= "V2 region" 'note= "V4 region" 'note= "V5 region 31-MAR-1994. Francis MJ; Synthetic. Sequence Aug 27 07:56 rotein Protein R51247; Region Region Region Region Matches 유 ð 

Fusaric acid resistance protein encoded by fdt2.

(first entry)

20-NOV-1991

Klebsiella oxytoca, strain HY-1.

28-FEB-1991; 103006. 28-FEB-1990; JP-045481. 18-FEB-1991; JP-044027.

04-SEP-1991.

EP-444664-A.

feline immunodeficiency virus (FIV) envelope protein from different strains and serotypes. The consensus sequence basedon these, is given in R51247. The synthetic FIV peptides of the invention were derived principally from a combination of the sequences of the FIV UK 8 and Petaluma isolates, a composite sequence of which is given in R51246. Variations in the sequence may occur between different strains or serotypes, isolates of different geographical origin or even between different isolates from the same host. nucleic acid - used to prepare prods. for combating or diagnosis Disclosure; Figure 2; 68pp; English. The sequences given in R51248-R51262 and R58584-85 represent the Feline immunodeficiency virus antigenic polypeptide(s) and Score 79; DB 10; Length 854; Pred. No. 2.84e+01; 3; Indels 2; Mismatches of feline immunodeficiency infection 8.98; Best Local Similarity 66.7%; 10; Conservative (PITM ) PITMAN MOORE INC 788 gilgiglgillilc 802 31 GILTVILGVLLIGC 45 20-SEP-1993; G01974. 21-SEP-1992; GB-019936. WPI; 94-118168/14. W09406471-A 31-MAR-1994 Francis MJ; Sequence Query Match Matches 셤 à

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Gaps

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Search completed: Tue Aug 27 08:09:18 1996

Job time : 29 secs.

5;

2; Gaps

16; Mismatches 36; Indels 8.9%; Score 79; DB 3; Length 234; 22.9%; Pred. No. 2.84e+01;

Best Local Similarity 22.9%; 16; Conservative

Matches

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20 SYTTAEEAAGIGILTVILG-VLLLIGCWYCRRRNGYRALMDKSLHVGTQCALTRRCPQEG 78

142 adaantaial 151

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| :: ::| 79 FDHRDSKVSL 88

ð

FIV PPR envelope protein sequence. Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS; T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein.

R51250 standard; peptide; 854 AA.

RESULT

08-0CT-1994 (first entry)

/note= "Hydrophobic leader peptide" Region 51..66

95..173

Region

/note= "Vl region" /note= "V2 region"

Protein 1/9......
//note= "Surface glycoprotein"
- -:-- 360..424

/note= "Transmembrane protein"

609..854

Protein

539..565 451..483

'note= "V5 region"

/note= "V4 region"

Region Region

'note= "V3 region"

Location/Qualifiers

Synthetic.

1..178

Peptide

The sequence was deduced from a clone isolated from a gene library prepd. from K. oxytoca. It is the 2nd of three proteins encoded by ORFs fdtl-fdt3 which are essential for fusaric acid resistance.

decomposing or detoxifying microorganisms e.g. Pseudomonas

Disclosure; Fig 7; 38pp; English.

cepacia.

Fusaric acid resistant genes - derived from fusaric acid

Y, Toyoda H, Utsumi R, Obata K;

(DAIK ) DAIKIN IND LTD. (SUNR ) SUNTORY LTD.

Shibano

WPI; 91-261442/36. N-PSDB; Q13370.

The genes can be introduced into plants in order to control plant diseases such as wilting disease caused by Fusarium fungi.

See also R13838-R13845.

234 AA;

Sequence Query Match

Aug 27 07:56

US-08-231-565A-2.rpr

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Aug 27 08:07:42 1996; MasPar time 6.40 Seconds 468.710 Million cell updates/sec Run on:

Tabular output not generated.

(1-118) from US08231565A.pep 889 >US-08-231-565A-2 Description: Perfect Score: Title:

1 MPREDAHFIYGYPKKGHGHS......NAPPAYEKLSAEQSPPPYSP 118 Sequence:

PAM 150 Gap 11 Scoring table:

82130 seqs, 25426960 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc 14:unrev Database:

Mean 39.239; Variance 79.176; scale 0.496 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	9.78e-155	4.15e-02	4.15e-02	4.15e-02	6.54e - 01	6.54e-01	1.18e + 00	1.58e+00	1.58e+00	1.58e+00	1.58e+00	2.11e+00
Description	melanoma antigen MAR	T-cell surface glyco	T-cell surface glyco	T-cell surface glyco	B-CAM protein - huma	Lutheran blood group	receptor protein kin	tyrosinase-related-p	tyrosinase-related p	protein-tyrosine-pho	protein-tyrosine-pho	tyrosinase-related p
ΩI	A55253	501347	502293	B28967	547272	551663	JQ1674	S41089	\$43510	D41214	C41214	S19243
DB	=	2	2	Ś	11	Ξ	6	12	12	10	10	4
Query Match Length DB	118	344	344	344	588	628	942	519	519	1557	1630	517
% Query Match	100.0	11.1	11.1	11.1	10.1	10.1	6.6	9.8	8.6	8.6	8.6	9.7
Score	889	66	66	66	90	8	88	87	87	87	87	98
Result No.	1	2	e	4	S	9	7	œ	6	10	11	12

2.11e+00	2.82e+00	2.82e+00	3.75e+00	3.75e+00		3.75e+00	4.98e+00	4.98e+00	4.98e+00	6.59e+00	6.59e+00	6.59e+00	6.59e+00	8.71e+00	8.71e+00	8.71e+00	8.71e+00	8.71e+00	8.71e+00	8.71e+00	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.5le+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.98e+01	1.98e+01	1.98e+01
meprin beta chain pr	probable membrane pr	H+-transporting ATPa	T-cell surface glyco	CDla protein - human	thymocyte antigen CD	e s	B-lymphocyte activat	meprin A (EC 3.4.24.	protein kinase - ric	interferon gamma rec	cytokine receptor co	probable membrane pr	protein-tyrosine-pho	dopamine receptor pr	aspartate chemorecep	aspartate chemorecep	/ polyprotein - fe		/ polyprotein - fe	hypothetical protein	VI protein - Miscant	MFS18 protein - maiz	myelin PO protein -	myelin protein - hum	fusion glycoprotein	integrin beta chain	fibronectin-binding	kinesin-related prot	integrin beta-4 chai	T-cell surface glyco	fusion glycoprotein	4D protein - fruit
A48040 mer	S32966 pro	PXBY1P H+-	HLHUCD T-c	A45911 CD]		A39957 T-c	S17291 B-1	S49383 mel	S50767 pro	A34368 int		S45389 pro		S44275 dog	QREBDT asp	A29053 asi	JQ2003 env	VCLJFP env	S23823 env				JH0252 my	S43191 mye	VGNZRL fu		S19702 fil		JN0786 int	B39957 T-		S17037 ncdD
704 12	320 10	918 1	229 2	306 5	127 5	127 5	306 12	700 11	124 9	477 5		1010 10	558 10	511 10	52 3	52 6	355 3	356 3	9 958	935 10	84 7	28 9	248 6	_	546 3	846 10	940 8	184 2	748 6	333 5	38 3	700 5
7. 6.	9.6	9.6	9.4	9.4	9.4	9.4	9,3	۳.		7.	9.5	.2	.2	9.1	9.1	۲.		9.1	9.1	9.1	8.9	6.	8.9	6.	6.	6.	6.	.9	.9	∞.	œ œ	œ.
98	82	82	84	84	84	84	83	83	83	85	8	82	82	81	81	81	81	81	81	81	19	79	79	79	19	79	79	79	79	78	78	78
13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

t_change	ns, P.F.; nberg, S.A. 19 elanoma ltrating into	3535	0; Gaps 0;
A55253 #type complete melanoma antigen MART-1 - human #formal name Homo sapiens #common name man 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change A55253	A55253 Kawakami, Y.; Eliyahu, S.; Delgado, C.H.; Robbins, P.F.; Rivoltini, L.; Topalian, S.L.; Miki, T.; Rosenberg, S.A. Proc. Natl. Acad. Sci. U.S.A. (1994) 91:3515-3519 Cloning of the gene coding for a shared human melanoma antigen recognized by autologous T cells infiltrating into	A35233 type mRNA 1-118 ##label KAW erences GB:U06452 #length 118 #molecular-weight 13157 #checksum 3535	Score 889; DB 11; Length 118; Pred. No. 9.78e-155; 0; Mismatches 0; Indels 0; Gaps
A55253 #type complete melanoma antigen MART-1 - human #formal name Homo sapiens #common name man 06-Feb-1995 #sequence_revision 06-Feb-1995 A55253	liyahu, S.; Delg ; Topalian, S.L. d. Sci. U.S.A. ( gene coding for nized by autolog	y bel KAW 52 olecular-weight	O D
A5523 #typ melanoma antige #formal name Ho 06-Feb-1995 #se A55253	A55253 Kawakami, Y.; E Kawakami, Y.; E Rivoltini, L. Proc. Natl. Aca Cloning of the antigen recog	cession A5253 ##status preliminary ##molecule_type_mRNA ##residues	Query Match 100.0%; Best Local Similarity 100.0%; Matches 118; Conservative
RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS	ACCESIONS RECERCIONE # authors # journal # title	#accession A55253 #fstatus prel #fstatus prel #fmolecule_type_mNuA #fresidues #fcross-references G SUMMARY #length 1	Query Match Best Local Similarity 100.0%, Matches 118; Conservative

1 mpredahfiygypkkghqhsyttaeeaaqigiltvilgvllligcwycrrrngyralmdk 60

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4;

Gaps

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Exon-intron organization and sequence comparison of human and Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L. Proc. Natl. Acad. Sci. U.S.A. (1988) 85:1615-1619 the authors translated the codon TAT for residue 99 #domain signal sequence flabel SIG\
#product T-cell surface glycoprotein CD2 flabel MAT
#length 344 #molecular-weight 38414 #checksum 4681 30-Jun-1989 #sequence\_revision 03-Jun-1993 #text\_change #formal name Homo sapiens #common\_name man 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change #length 344 #molecular-weight 38325 #checksum 4974 formal name Mus musculus #common name house mouse 198 pekglsf-yvtvgvgag-glllvll-valfifc-ickrrkrnrrrkdeelei 245 198 pekglsf-yvtvgvgag-glllvll-valfifc-ickrrkrnrrrkdeelei 245 13 PKKGHGHSYTTAEEAAGIGILTVILGVLLLIGCWYCRRRNGYRALMDKSLHV Score 99; DB 5; Length 344; Pred. No. 4.15e-02; 9; Mismatches 18; Indels -cell surface glycoprotein T11 (CD2) - mouse 11.1%; Score 99; DB 5; Length 344; Campbell, I.G. submitted to the EMBL Data Library, July 1994 9; Mismatches 18; Indels #superfamily T-cell surface glycoprotein CD2
glycoprotein; T-cell #superfamily T-cell surface glycoprotein CD2 ##residues 1-344 ##label DIA ##cross-references GB:M19807; GB:J03622; GB:J03623 Best Local Similarity 40.4%; Pred. No. 4.15e-02; murine Tll (CD2) genes. fcross-references MUID:88144486 #type complete #type complete B-CAM protein - human ##cross-references EMBL:Y00023 preliminary Query Match 11.1%; Best Local Similarity 40.4%; 21; Conservative 21; Conservative 31-Dec-1993 B28967 06-Jan-1995 glycoprotein ##molecule\_type mRNA ##molecule type mRNA A28967 547272 B28967 S47272 #map\_position 3 CLASSIFICATION #s CLASSIFICATION #submission ##status #accession Query Match #accession authors ACCESSIONS REFERENCE #authors iournal Matches ACCESSIONS #title 23-344 REFERENCE GENETICS KEYWORDS ORGANISM KEYWORDS ORGANISM SUMMARY SUMMARY FEATURE RESULT RESULT ENTRY 셤 à ð 4; molecular cloning, chromosome assignment and cell surface Clayton, L.K.; Sayre, P.H.; Novotny, J.; Reinherz, E.L. Eur. J. Immunol. (1987) 17:1367-1370 Murine and human T11 (CD2) cDNA sequences suggest a common product T-cell surface glycoprotein CD2 #label MAT\
#domain extracellular #label EXT\ Sewell, W.A.; Brown, M.H.; Owen, M.J.; Fink, P.J.; Kozak, 1 MPREDAHFIYGYPKKGHGHSYTTAEEAAGIGILTVILGVLLLIGCWYCRRNGYRALMDK 60 CD2 antigen; 711 protein set precured - mouse #formal name Mus musculus #common name house mouse 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Sep-1994 Gaps #formal\_name Mus musculus #common name house mouse
01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change The murine homologue of the T lymphocyte CD2 antigen: #length 344 #molecular-weight 38400 #checksum 4741 4; T-cell surface glycoprotein CD2 precursor - mouse 198 pekglsf-yvtvgvgag-glllvll-valfifc-ickrrkrnrrrkdeelei 245 T-cell surface glycoprotein CD2 precursor - mouse T-lymphocyte antigen CD2 13 PKKCHCHSYTTAEEAAGIGILTVILGVLLLIGCWYCRRNGYRALMDKSLHV 64 not compared with conceptual translation 9; Mismatches 18; Indels DB 5; Length 344; CLASSIFICATION #superfamily T-cell surface glycoprotein CD2 #domain signal sequence #label SIG\ domain transmembrane #label TMM\ #domain intracellular #label INT C.A.; Crumpton, M.J. Eur. J. Immunol. (1987) 17:1015-1020 Query Match 11.1%; Score 99; DB 5; Lk Best Local Similarity 40.4%; Pred. No. 4.15e-02; Matches 21; Conservative 9; Mismatches 18: glycoprotein; transmembrane protein signal transduction mechanism. fcross-references MUID:88004738 #type complete #type complete ##molecule\_type mRNA #fresidues 1-344 ##label CLA 1-344 ##label SEW ##cross-references EMBL:X06143 #cross-references MUID:87276135 18-Jun-1993 expression. ##molecule\_type mRNA 501347 502293

##residues

204-228

23-344 23-203

KEYWORDS FEATURE

229-344

SUMMARY

ALTERNATE NAMES

RESULT ENTRY TITLE

셤 ð ORGANISM

#authors | journal

#title

ACCESSIONS

REFERENCE

4;

Gaps

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##residues

##status #accession

ALTERNATE NAMES

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#authors #journal

#title

ACCESSIONS

REFERENCE

1-588 ##label CAM

##residues

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1-942 ##label CHA

##residues

##cross-references GB:L00670

Biochim. Biophys. Acta (1994) 1217:317-321 Molecular cloning and functional analysis of a cDNA coding

#journal #title

#authors

REFERENCE

Yokoyama, K.; Suzuki, H.; Yasumoto, K.; Tomita, Shibahara, S.

for human DOPAchrome tautomerase/tyrosinase-related

ä :: Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Spurr, N.K.; Warne, D.; Barclay, A.N.; Anstee, D.J. immunoglobulin superfamily, is widely expressed in human tissues and is developmentally regulated in human liver. The Lutheran blood group glycoprotein, a new member of the The TWK1 gene from Arabidopsis codes for a protein with structural and biochemical characteristics of a receptor !formal name Arabidopsis thaliana #common\_name mouse-ear Gaps Gaps Lutheran blood group glycoprotein precursor - human #formal name Homo sapiens #common\_name man 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change Chang, C.; Schaller, G.E.; Patterson, S.E.; Kwok, S.F.; Meyerowitz, E.M.; Bleecker, A.B. J01674 #type complete receptor protein kinase TMK1 (EC 2.7.1.-) precursor -##cross-references EMBL:X83425 Y #length 628 #molecular-weight 67374 #checksum 416 ##cross-references EMBL:X80026 Y #Length 588 #molecular-weight 63566 #checksum 255 ä :: submitted to the EMBL Data Library, December 1994 Query Match 10.1%; Score 90; DB 11; Length 588; Best Local Similarity 34.4%; Pred. No. 6.54e-01; Matches 11; Conservative 12; Mismatches 8; Indels Query Match 10.1%; Score 90; DB 11; Length 628; Best Local Similarity 34.4%; Pred. No. 6.54e-01; 8; Indels 11; Conservative 12; Mismatches 544 tsqagvavmavavsvgllllvvavfycvrrkg 575 544 tsqaqvavmavavsvgllllvvavfycvrrkg 575 Plant Cell (1992) 4:1263-1271 23 TAEEAAGIGILTVILGVLLLI-GCWYCRRNG 53 23 TAEEAAGIGILIVILGVLLI-GCWYCRRNG 53 #type complete 1-628 ##label PAR Arabidopsis thaliana protein kinase. preliminary 01-Sep-1995 09-Sep-1994 ##molecule\_type DNA ##molecule\_type DNA cress 551663 551663 JQ1674 S51663 301674 J01674 JQ1674 ##residues #description submission #status #accession #authors #author*e* #journal ACCESSIONS ACCESS IONS Matches title TITLE ORGANISM REFERENCE REFERENCE ORGANISM SUMMARY SUMMARY RESULT RESULT ENTRY TITLE ENTRY DATE 셤 ð 음 ð

#product receptor protein kinase TMK1 #status predicted <u>;</u>; ; Molecular characterization of a human tyrosinase-related-protein-2 cDNA. Patterns of expression #domain signal sequence #status predicted #label SIGN #binding\_site carbohydrate (Asn) (covalent) #status Gaps Gaps glycoprotein; phosphotransferase; transmembrane protein #formal name Homo sapiens #common name man 25-Dec-I994 #sequence\_revision 10-Nov-1995 #text\_change #formal name Homo sapiens #common\_name man 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change #region serine/threonine protein kinase homology\
#region serine/threonine protein kinase homology\ predicted #length 942 #molecular-weight 102387 #checksum 2851 Bouchard, B.; del Marmol, V.; Jackson, I.J.; Cherif, #length 519 #molecular-weight 59145 #checksum 989 1; 4; Indels 1; 9.8%; Score 87; DB 12; Length 519; 5.3%; Pred. No. 1.58e+00; 9.9%; Score 88; DB 9; Length 942; 37.5%; Pred. No. 1.18e+00; 11; Mismatches 10; Indels #domain transmembrane #label TMM\ tyrosinase-related-protein-2 - human tyrosinase-related protein 2 - human Eur. J. Biochem. (1994) 219:127-134 10; Mismatches 477 mgtlvalvglfvllaflqyrrlrkgytplmethl 510 30 IGILTVILGVLLLIGCWYCRR-RNGYRALMDKSL 62 #type complete #type complete 1-519 ##label BOU in melanocytic cells. 491 qllsifl-iqllvfcwykkrqkrf 513 31 GILTVILGVLLIGCWYCRRRNGY 54 #label MAT\ preliminary Dubertret, L. Query Match 9.9%; Best Local Similarity 37.5%; Query Match
Best Local Similarity 35.3%;
Matches 12; Conservative 9; Conservative 10-Nov-1995 S41089 03-Mar-1995 ##molecule\_type mRNA \$43510 \$43510 541089 S41089 S41089 86, 99, 158, 164, 171, ##residues 363, 533, 587 ##status #accession #authors # journal FEATURE 1-22 23-942 ACCESSIONS ACCESSIONS 480 - 503#title REFERENCE ORGANISM ORGANISM KEYWORDS SUMMARY SUMMARY RESULT RESULT TITLE ENTRY TITLE ENTRY DATE DATE 쇰 g ð ð

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ï  $\mbox{\$active}$  site Cys (phosphocysteine intermediate)  $\mbox{\$status}$  predicted\ ä are preliminary; not compared with conceptual translation fdomain protein-tyrosine-phosphatase homology flabel Gaps receptor-like, short splice form precursor - fruit fly Two Drosophila receptor-like tyrosine phosphatase genes expressed in a subset of developing axons and pioneer neurons in the embryonic CNS. Gaps #formal\_name Drosophila melanogaster 28-May-1992 #sequence\_revision 28-May-1992 #text\_change receptor-like, long splice form precursor - fruit fly (Drosophila melanogaster) Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W. Cell (1991) 67:661-673 #length 1557 #molecular-weight 177147 #checksum 4501 #binding\_site substrate phosphate (Arg) #status #length 519 #molecular-weight 59145 #checksum 989 #superfamily protein-tyrosine-phosphatase homology ä ä. protein-tyrosine-phosphatase (EC 3.1.3.48) 10D, Score 87; DB 10; Length 1557; Pred. No. 1.58e+00; C41214 #type complete protein-tyrosine-phosphatase (EC 3.1.3.48) 10D, Score 87; DB 12; Length 519; 11; Mismatches 10; Indels 7; Mismatches 19; Indels Db 1184 ysfpiqtd-qdntslivaitvp-ltiil-vllvtlifykrrrnncr 1226 nucleotide sequence is not given Pred. No. 1.58e+00; 477 mgtlvalvglfvllaflqyrrlrkgytplmethl 510 30 IGILTVILGVLLIGGWYCRR-RNGYRALMDKSL 62 phosphoric monoester hydrolase (Drosophila melanogaster) #type complete 1-1557 ##label YAN 1-519 ##label YOK ##cross-references EMBL:D17547 #cross-references MUID:92034988 ##cross-references GB:M80465 preliminary Query Match
9.8%;
Best Local Similarity 37.0%;
Matches 17; Conservative Query Match 9.8%; Best Local Similarity 35.3%; 12; Conservative 25-Aug-1995 PTP1\ protein-2 ##molecule\_type\_mRNA #molecule type mRNA 543510 D41214 A41214 D41214 D41214 # residues #residues CLASSIFICATION #status ##status faccession #accession Query Match fnote 1295-1515 10 Ξ **f**authors #journal ACCESSIONS Matches #title REFERENCE ORGANISM KEYWORDS 1473 SUMMARY FEATURE 1467 RESULT ENTRY SUMMARY RESULT ENTRY TITLE TITLE 셤 ô ð

US-08-231-565A-2.pg Aug 27 07:56

Jackson, I.J.; Chambers, D.M.; Tsukamoto, K.; Copeland, N.G.; ä #active\_site Cys (phosphocysteine intermediate) #status Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a subset of developing axons and pioneer 18 #domain protein-tyrosine-phosphatase homology #label Gaps TRP-2, maps to and #formal name Drosophila melanogaster
28-May-1992 #sequence\_revision 12-Jun-1992 #sext\_change 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change #checksum 8804 #binding\_site substrate phosphate (Arg) #status #length 517 #molecular-weight 58569 #checksum 6717 Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, Cell (1991) 67:661-673 #superfamily protein-tyrosine-phosphatase homology phosphoric monoester hydrolase #formal name Mus musculus #common name house mouse 3; Length 1630; Indels Db 1184 ysfpiqtd-qdntslivaitvp-ltiil-vllvtlifykrrrnncr 1226 Length 517; Gilbert, D.J.; Jenkins, N.A.; Hearing, V. EMBO J. (1992) 11:527-535 10 YGYPKKGHGHSYTAAEBAAGIGILTVILGVLLLIGCWYCRRRNGYR 55 tyrosinase-related protein TRP-2 - mouse #length 1630 #molecular-weight 184861 #superfamily monophenol monooxygenase 7; Mismatches 19; A second tyrosinase-related protein, Query Match 9.8%; Score 87; DB 10; Best Local Similarity 37.0%; Pred. No. 1.58e+00; Matches 17; Conservative 7; Mismatches 19. Query Match 9.7%; Score 86; DB 4; Lv Best Local Similarity 41.2%; Pred. No. 2.11e+00; mutated at the mouse slaty locus, neurons in the embryonic CNS. #type complete 1-1630 ##label YAN 1-517 ##label JAC #cross-references EMBL:X63349 #cross-references MUID:92034988 #cross-references GB:M80465 predicted\ fcross-references MUID:92164640 preliminary predicted preliminary 25-Aug-1995 12-Apr-1995 S19243 ##molecule\_type mRNA ##molecule\_type mRNA A41214 519243 C41214 C41214 519243 ##residues ##residues CLASSIFICATION CLASSIFICATION #status #status #accession 1295-1515 12 #authors authors | journal | journal **ACCESSIONS** ACCESSIONS #title REFERENCE #title REFERENCE ORGANISM ORGANISM KEYWORDS 1473 1467 SUMMARY SUMMARY RESULT ENTRY TITLE DATE ð

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##status #accession

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SUMMARY

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REFERENCE

3

Gaps

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Yeast plasma membrane ATPase is essential for growth and has homology with (Na(1+) and K(1+)), K(1+)- and Ca reference but was verified by personal communication the species of yeast is not given explicitly in this regulate intracellular pH and ion balance and to generate the electrochemical gradient that drives nutrient uptake. #domain transmembrane #status predicted #label TM1\ #domain transmembrane #status predicted #label TM2\ #domain transmembrane #status predicted #label TM4\ #domain transmembrane #status predicted #label TM5\ #domain transmembrane #status predicted #label TM6\ #domain transmembrane #status predicted #label TM7\ #domain transmembrane #status predicted #label TM8\ #domain transmembrane #status predicted #label TM3 #length 320 #molecular-weight 35986 #checksum 4017 ATP; hydrogen ion transport; hydrolase; phosphorylation; H+-transporting ATPase (EC 3.6.1.35) 1, plasma membrane 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change This ATPase transports protons across the plasma membrane to #active\_site Asp (aspartylphosphate intermediate) #domain transmembrane #status predicted #label #domain transmembrane #status predicted #label #domain transmembrane #status predicted #label #molecular-weight 99530 #checksum 3552 #superfamily Na+/K+-transporting ATPase alpha chain Serrano, R.; Kielland-Brandt, M.C.; Fink, G.R. Nature (1986) 319:689-693 Length 320; 9.6%; Score 85; DB 1; Length 918; 4; Indels US-08-231-565A-2.rpr formal name Saccharomyces cerevisiae Score 85; DB 10; 1 Pred. No. 2.82e+00; yeast (Saccharomyces cerevisiae) 8; Mismatches #type complete #status predicted transmembrane protein 1-918 ##label SER from the author 287 fgvlsnilvvpfymvgcswyirkw 310 30 IGILTVILGV-LLLIGC-WYCRRR 51 #cross-references EMBL:X03534 #cross-references MUID:86146844 membrane protein (2+)-ATPases Best Local Similarity 41.7%; #status absent 14-Sep-1994 10; Conservative #length 918 proton pump LISTA: PMA1 ##molecule\_type\_DNA A25823 PXBY1P A25823 #map\_position 2R KEYWORDS mer #map position ##residues ALTERNATE NAMES CLASSIFICATION Aug 27 07:56 #accession Query Match Query Match 15 authors fintrons journal 116-137 141-163 292-314 257-273 285-304 325-347 719-743 755-777 825-846 860-882 162-178 ACCESSIONS Matches REFERENCE #title ORGANISM GENETICS KEYWORDS COMMENT FEATURE SUMMARY FEATURE SUMMARY RESULT ENTRY TITLE 음 ð ð Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; ä The complete sequence of a 19,482 bp segment located on the right arm of chromosome II from Saccharomyces cerevisiae, 532966 Cloning, expression, and chromosomal localization of the Gaps probable membrane protein YBR265w - yeast (Saccharomyces meprin beta chain precursor - mouse formal name Mus musculus fcommon name house mouse 02-Jun-1995 fsequence\_revision 02-Jun-1995 ftext\_change 07-Jul-1995 30-Sep-1993 #sequence revision 30-Sep-1993 #text change \*submission submitted to the Protein Sequence Database, August 1994 Gorbea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Bond, J.S. J. Biol. Chem. (1993) 268:21035-21043 #length 704 #molecular-weight 79585 #checksum 7013 ä translation of nucleotide sequence not given Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M. Yeast (1993) 9:189-199 Length 704; 14; Mismatches 14; Indels CLASSIFICATION #superfamily MAM homology; astacin homology #domain astacin homology #label AST\ 648 krgstrdtvijavsstvtvfavml-iitlvsv-yctrrk-yr 686 |:| :: :::|:| || ||: || 14 KKGHGHSYTTAÆEAAGIGILITVILGVILLIGCWYCRRNGYR 55 formal\_name Saccharomyces cerevisiae #domain MAM homology #label MAM Score 86; DB 12; Pred. No. 2.11e+00; 30 IGILTVILGVLLLIGGWYCRR-RNGYRALMDKSL 62 hypothetical protein YBR1734 mouse meprin beta subunit. #type complete #type complete ##residues 1-320 ##label DOI ##cross-references EMBL:X70529 ##notes ##molecule\_type DNA ##residues 1-320 ##label AIG ##molecule\_type\_mRNA ##residues 1-704 ##label GOR ##cross-references EMBL:236134 #cross-references GB:L15193 preliminary Query Match 9.7%; Best Local Similarity 26.2%; S32966; S46146 11; Conservative 24-Feb-1995 cerevisiae) Doignon, F ##molecule\_type DNA S32966 S29348 \$45940 A48040 A48040 A48040 A48040

ALTERNATE NAMES

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RESULT

ENTRY TITLE #accession

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э; 4; Gaps Best Local Similarity 34.1%; Pred. No. 2.82e+00; Matches 15; Conservative 11; Mismatches 14; Indels

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Search completed: Tue Aug 27 08:08:31 1996 Job time: 49 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Tue Aug 27 08:07:11 1996; MasPar time 5.49 Seconds 373.873 Million cell updates/sec Run on:

Tabular output not generated.

1 MPREDAHFIYGYPKKGHGHS........NAPPAYEKLSAEQSPPPYSP 118 >US-08-231-565A-2 (1-118) from US08231565A.pep 889 Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

49340 seqs, 17385503 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Database:

Mean 40.794; Variance 65.678; scale 0.621 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	OI	Description	Pred. No.
1	66	11.11	344	2	CD2 MOUSE	T-CELL SURFACE ANTIGE	2.97e-03
7	88	6.6	942	00	TMKI ARATH	PUTATIVE RECEPTOR PRO	1.69e-01
m	87	9.8	519	œ	TYR2 HUMAN	DOPACHROME TAUTOMERAS	2.41e - 01
4	87	8.6	1630	9	PTP1_DROME	PROTEIN-TYROSINE PHOS	2.41e - 01
2	86	9.7	517	00	TYR2 MOUSE	DOPACHROME TAUTOMERAS	3.41e - 01
9	82	9.6	320	6	YB9K YEAST	HYPOTHETICAL 36.0 KD	4.82e-01
7	82	9.6	918	-	ATH1 YEAST	PLASMA MEMBRANE ATPAS	4.82e-01
œ	84	9.4	327	7	CD1A HUMAN	T-CELL SURFACE GLYCOP	6.78e-01
6	83	9.3	306	7	CD80 MOUSE	T LYMPHOCYTE ACTIVATI	9.52e-01
10	85	9.5	477	4	INGR MOUSE	INTERFERON-GAMMA RECE	1.33e+00
11	82	9.5	897	7	CYRB HUMAN	CYTOKINE RECEPTOR COM	1.33e+00
12	82	9.5	1010	Φ	YBK6 YEAST	HYPOTHETICAL 111.7 KD	1.33e+00
13	81	9.1	511	m	DOPR DROME	DOPAMINE RECEPTOR PRE	1.86e+00

1.86e + 00	1.86e + 00	1.86e+00	1.86e+00	1.86e+00	2.58e+00	3.57e+00	3.57e+00	3.57e+00	3.57e+00	3.57e+00	3.57e+00	4.93e+00	4.93e+00	4.93e+00	4.93e+00	4.93e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	6.78e+00	9.29e+00	9.29e+00	9.29e+00	9.29e+00	
METHYL-ACCEPTING CHEM	PEPTIDE TRANSPORTER P	ENVELOPE POLYPROTEIN	ENVELOPE POLYPROTEIN	PUTATIVE CLATHRIN-COA	HYPOTHETICAL 33.9 KD	MFS18 PROTEIN PRECURS	MYELIN PO PROTEIN PRE	FUSION GLYCOPROTEIN P	INTEGRIN BETA-SUBUNIT	ENVELOPE POLYPROTEIN	KINESIN-LIKE PROTEIN	BETA-ELICITIN DRE-BET	T-CELL SURFACE GLYCOP	FUSION GLYCOPROTEIN P	CLARET SEGREGATIONAL	VACB PROTEIN.	BETA-ELICITIN CRYPROG	CYTOCHROME B5.	MYELIN PO PROTEIN PRE	MYELIN PO PROTEIN PRE	FRUCTOSE-BISPHOSPHATE	HEPATOCYTE NUCLEAR FA	HEPATOCYTE NUCLEAR FA	M POLYPROTEIN PRECURS	M POLYPROTEIN PRECURS	M POLYPROTEIN PRECURS	CELL DIVISION PROTEIN	GRANATICIN POLYKETIDE	T-CELL SURFACE GLYCOP	VACB PROTEIN.	PLASMA MEMBRANE ATPAS	
MCP2 SALTY	PTR2 CANAL	ENV FIVU2	ENV FIVPE	VPP T CAEEL	YAC2_SCHPO	MF18 MAIZE	MYP 0 HUMAN	VCLF RINDL	ITBX DROME	ENV FIVSD	BIMC EMENI	ELIB PHYDR	CD1B HUMAN	VGLF TRTV	NCD DROME	VACE SHIFL	ELIB PHYCR	CYB5 YEAST	MYPO RAT	MYPO MOUSE	ALF TRYBB	HNF4 RAT	HNF4 HUMAN	VGLM PUUMH	VGLM PUUMK	VGLM PUUMP	FTSK ECOLI	CYPK STRCM	CD4 CANFA	VACE ECOLI	ATHP_ZYGRO	
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9.1	9.1	9.1	9.1	9.1	0.6	6.8	8.9	8.9	8.9	6.8	8.9	8.8	8.8	8.8	80	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8,5	8.5	8.5	8.5	
81	81	81	81	81	80	79	79	79	79	79	79	78	78	78	78	78	11	11	11	11	11	11	11	11	11	11	11	16	16	16	16	
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### ALIGNMENTS

RESULT ID C	CD2 MOUSE	STA	STANDARD;	;g	PRT;	344 AA.	AA.	
금	PU892U; 01-NOV-1988	(REL.	60	CREATED	_			
υL	01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)	(REL.	60	LAST SE	DUENCE U	PDAT	Ξ)	
DI	01-FEB-1995	(REL.	31,	LAST AN	NOTATION	UPD	ATE)	
E	T-CELL SURFACE ANTIGEN CD2 PRECURSOR (T-CELL SURFACE ANTIGEN	CE ANT	ICEN	N CD2 PR	ECURSOR	(T-C	ELL SURFACE	ANTIGEN
띰	T11/LEU-5) (LFA-2) (LFA-3 RECEPTOR).	LFA-2)	3	PA-3 REC	EPTOR).			
SO	MUS MUSCULUS (MOUSE).	SHOM)	(i)					
ဗ	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	ETAZOA	Ö	HORDATA;	VERTEBR	ATA;	TETRAPODA;	MAMMALIA;
ဗ	EUTHERIA; RODENTIA.	DENTIA						
RN	Ξ							
RP	SEQUENCE FROM N.A.	M N.A.						
RC SC	STRAIN-B10.A;							
æ	MEDLINE; 87276135.	76135.						
æ	SEWELL W.A., BROWN M.H., FINK P.J., KOZAK C.A., CRUMPTON M.J.;	BROWN	Σ	A., FINK	P.J., K	OZAK	C.A., CRUM	PTON M.J.;
RL	EUR. J. IMMUNOL. 17:1015-1020(1987)	NOL. 1	7:10	015-1020	(1987).			
æ	[2]							
RP.	SEQUENCE FROM N.A.	M N.A.						
æ	MEDLINE; 88004738.	04738.						
æ	CLAYTON L.K., SAYRE P.H., NOVOTNY J., REINHERZ E.L.;	, SAYR	ם	.H., NOV	JINY J.,	Æ	NHERZ E.L.;	
Æ	EUR. J. IMMUNOL. 17:1367-1370(1987).	NOL. 1	7:13	367-1370	(1987).			
S	[3]							
RP	SEQUENCE FROM N.A.	M N.A.						
æ	MEDLINE; 88144486.	44486.						
RA.	DIAMOND D.J., CLAYTON L.K., SAYRE P.H., REINHERZ E.L.;	, CLAY	ΙΟ̈́Ι	L.K., S.	AYRE P.H	æ ;	EINHERZ E.L	•
: [	PROC. NATL.	ACAD.	SCI	U.S.A.	85:1615	-161	9(1988).	410000
ဗ	-:- FUNCTION: CD2 INTERACTS WITH LIMPHOCITE FUNCTION-ASSOCIATED	: CD7	Z	ERACTS W	TEH LYMP	HOC.	TE FUNCTION	-ASSOCIATED

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RA CHANG C., SCHALLER G.E., PATTERSON S.E., KWOK S.F., RA MEYEROWITZ E.M., BLECKER A.B.; RL PLANT CELL 4:1263-1271(1992).		KW         TRANSMEMBRANE;         RECEPTOR;         GLYCOPROTEIN;         SIGNAL;           FT         LEUCINE-REPEAT;         PHOSPHORYLATION.           FT         CHAIN         24         482         POTENTIAL.           FT         CHAIN         24         482         EXTRACELLUIAR (POTENTIAL).           FT         DOMAIN         24         482         EXTRACELLUIAR (POTENTIAL).           FT         DOMAIN         584         692         PROTENTIAL.           FT         NP         BIND         594         PROTENTIAL.           FT         NP         BIND         594         602         ATP (BY SIMILARITY).           FT         ACT_SITE         717         717         BY SIMILARITY.           FT         CARBOHYD         59         90         POTENTIAL.           FT         CARBOHYD         158         158         POTENTIAL.           FT         CARBOHYD         164         POTENTIAL.         FT           FT         CARBOHYD         285         POTENTIAL.         FT           FT         CARBOHYD         363         POTENTIAL.         FT           FT         CARBOHYD         397         POTENTIAL.         FT	SEQUENCE 942 AA, 102387 MM Query Match 9.9%; S Best Local Similarity 37.5%; P Matches 9; Conservative 1 491 gllsifl-igllvfcwykkrqkrf    ::::	RESULT 3  ID TYR2_HUMAN STANDARD; PRT; 519 AA.  AC P40126;  DT 01-FEB-1995 (REL. 31, CREATED)  DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  DE DOPACHROME TAUTOMERASE PRECURSOR (EC 5.3.3.12) (DT) (DCT) (DOPACHROME DE DELTA-ISOMERASE) (TYROSINASE-RELATED PROTEIN 2) (TRP2).  GR TYRP2.  OC EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  OC EUTHERIA; PRIMATES.  RN 111  RP SEQUENCE FROM N.A.  RX MEDILINE; 94198295.
	CC SIGNALLING FUNCTION.  CC -!- SUBCELULILAR LOCATION.  CC -!- SUBCELULILAR LOCATION. TYPE I MEMBRANE PROTEIN.  CC -!- SIMILARITY: BELONGS TO THE IMMUNGLOBULIN SUPERFAMILY.  DR EMBL; Y00023, Y00023.  DR EMBL; M19799, M19799.  DR EMBL; M19803; M19803.  DR EMBL; M19805; M19805.  DR EMBL; M19805; M19805.  DR EMBL; M19807; M19807.  DR PIR; S02293; S02293.  DR PIR; S02967; B28967.	HSSP; IMMUN CELL SIGNP CHAIN CHAIN CHAIN DOMAI DOMAI DOMAI DOMAI DOMAI DOMAI DOMAI DOMAI DOMAI CARBG CARBG CARBG CARBG CARBG CARBG CARBG CARBG CONFI CONFI	SEQUENCE 344 AA; 38414 MM; 619144 CN; ODERY MATCH 11.1%; Score 99; DB 2; Best iocal Similarity 40.4%; Pred. No. 2.97e-0 Matches 21; Conservative 9; Mismatches 198 pekglsf-yvtvgvgag-glllvll-valfifc-ickrrk 11	RESULT 2  ID TMK1 ARATH STANDARD; PRT; 942 AA.  AC 843299; DT 01-00V-1995 (REL. 32, CREATED) DT 01-0VV-1995 (REL. 32, LAST SEQUENCE UPDATE) DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) DF PUTATIVE RECEPTOR PROTEIN KINASE TWKI PRECURSOR (EC 2.7.1).  GN TWK1  CARAIDOPSIS THALIANA (MOUSE-EAR CRESS).  CEMRARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; CC CAPPARALES; CRUCIFERAE.  RN [1] RP SEQUENCE FROM N.A.  RY STRAIN-CY. COLUMBIA; RX MYDI,NNE: 93076110.

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PIR; C41214; C41214.
PIR; D41214; D41214.
PIR; A41215; A41215.
HSSP; P02751; ITTF.
FLYBASE; FBGN0004370; PTP10D. 955 1048 11189 1532 1532 169 169 212 222 229 229 289 317 471 512 533 588 668 687 CELL 67:661-673(1991). CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD **TRANSMEM** CARBOHYD REPEAT. SIGNAL DOMAIN CHAIN ä Gaps PROTEIN-TYROSINE PHOSPHATASE 10D PRECURSOR (EC 3.1.3.48) (RECEPTOR-LINKED PROTEIN-TYROSINE PHOSPHATASE 10D). YOKOYAMA K., SUZUKI H., YASUMOTO K.I., TOMITA Y., SHIBAHARA S.; BIOCHIM. BIOPHYS. ACTA 1217:317-321(1994). -!- CATALYTIC ACTIVITY: DOPACHROME = 5,6-DIHYDROXYINDOLE-2--!- PATHWAY: MELANIN BIOSYNTHESIS. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MELANOSOMAL. -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. EMBL; D17547; D17547. :: LUMENAL, MELANOSOME (POTENTIAL) Score 87; DB 8; Length 519; Pred. No. 2.41e-01; Indels -!- COFACTOR: CONTAINS TWO ZINC ATOMS (BY SIMILARITY) PIR, \$43510; \$43510.

MIM; 191275; 11TH EDITION.

PROSITE; PS00497; TYROSINASE 1.

PROSITE; PS00498; TYROSINASE 2.

ISOMERASE; ZINC; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE;

MELANIN BIOSYNTHESIS. ZINC A (BY SIMILARITY).
ZINC A (BY SIMILARITY).
ZINC B (BY SIMILARITY).
ZINC B (BY SIMILARITY).
ZINC B (BY SIMILARITY).
ZINC B (BY SIMILARITY). CYTOPLASMIC (POTENTIAL) DOPACHROME TAUTOMERASE. DROSOPHILA MELANOGASTER (FRUIT FLY). EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA 01-UN-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE) 11; Mismatches 477 mgtlvalvglfvllaflqyrrlrkgytplmethl 510 PRT; 1630 AA 30 IGILTVILGVLLIGCWYCRR-RNGYRAIMDKSL 62 59145 MW; 1422986 CN; POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL POTENTIAL TIAN S.-S., TSOULFAS P., ZINN K.; CELL 67:675-685(1991). Query Match 9.8%; Best Local Similarity 35.3%; Matches 12; Conservative STANDARD; 170 178 178 178 237 300 342 342 377 519 AA; SEQUENCE FROM N.A. MEDLINE; 92034989. [2] SEQUENCE FROM N.A. TISSUE=EMBRYO; MEDLINE; 92034988. CARBOXYLATE. 24 24 473 494 189 220 220 369

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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -!- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO. -!- SIMILARITY: CONTAINS ONE PROTEIN-TYROSINE PHOSPHATASE DOMAIN AND 12 FIRRONDCTIN TYPE III-LIKE DOMAINS.
-!- ALTERNATIVE PRODUCTS: TWO ISOFORMS THAT DIFFER IN THEIR C-TERMINAL TAILS ARE PRODUCED BY ALTERNATIVE SPLICING.
EMBL, M80538; M80538.
EMBL, M80465; M80465. PROSITE; PS00383; TYR PHOSPHATASE. TRANSMEMBRANE; HYDROLĀSE; DUPLICATION; SIGNAL; ALTERNATIVE SPLICING; PROTEIN-TYROSINE PHOSPHATASE 10D -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 = PROTEIN-TYROSINE PHOSPHATASE. EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL) YANG X., SEOW K.T., BAHRI S.M., OON S.H., CHIA W.; FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. TYPE-III TYPE-III 'IBRONECTIN TYPE-III FIBRONECTIN TYPE-III FIBRONECTIN TYPE-III FIBRONECTIN TYPE-III FIBRONECTIN TYPE-III FIBRONECTIN TYPE-II1 FIBRONECTIN FIBRONECTIN FIBRONECTIN POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL OTENTIAL OTENTIAL POTENTIAL POTENTIAL POTENTIAL OTENTIAL POTENTIAL POTENTIAL PROTEIN TYROSINE + ORTHOPHOSPHATE.

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EMBL; X63349; X63349.

PIR; S19243; S19243. PROSITE; PS00497; TYROSINASE 1. PROSITE; PS00498; TYROSINASE 2. ISOMERASE; ZINC; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE;

MELANIN BIOSYNTHESIS, DISEASE MUTATION.

DOPACHROME TAUTOMERASE. LUMENAL MELANOSOME (POTENTIAL).

CYTOPLASMIC (POTENTIAL)

POTENTIAL.

491

TRANSMEM

DOMAIN DOMAIN METAL METAL METAL

CHAIN

24 24 473 492 1189 211 220 369

ZINC A (BY SIMILARITY).
ZINC A (BY SIMILARITY).
ZINC A (BY SIMILARITY).
ZINC B (BY SIMILARITY).
ZINC B (BY SIMILARITY).
ZINC B (BY SIMILARITY).

POTENTIAL.

POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.

CARBOHYD

METAL METAL METAL

CARBOHYD CARBOHYD CARBOHYD R -> 0 (IN SLATY).

58569 MW; 1366219 CN;

517 AA;

CARBOHYD CARBOHYD SEQUENCE

VARIANT

CARBOHYD

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1135 1135 POTENTIAL. 1194 1194 POTENTIAL. 1467 1467 BY SIMILARITY. 1558 1557 GQQQQLDENG -> DDI 1558 1630 MISSING (IN SHORT) 1125 1125 Y -> YQ (IN REF. In 6 1167 IG -> YP (IN REF. In 7 1172 In 7 In	Query Match 9.8%; Score 87; DB 6; Length 1630; Best Local Similarity 37.0%; Pred. No. 2.41e-01; Matches 17; Conservative 7; Mismatches 19; Indels 3; Gaps 3;	Db 1184 ysfpiqtd-gdntslivaitvp-ltiil-vllvtlifykrrrnncr 1226  ::  :  :   :	ID TYRZ MOUSE STANDARD; PRT; 517 AA.  AC P29812; DT 01-ARR-1993 (REL. 25, CREATED) DT 01-ARR-1993 (REL. 25, LAST SEQUENCE UPDATE) DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) DE DOPACHROME TAUTOWERASE PRECURSOR (EC 5.3.3.12) (DT) (DCT) (DOPACHROME DE DELTA-ISOMERASE) (TYROSINASE-RELATED PROTEIN 2) (TRP-2) (TRP2) (SLATY DE LOCUS PROTEIN).  CAN TYRD OR TYRD-2	MUS MUSCU EUKARYOTA EUTHERIA; [1] SEQUENCE		
8						

ï Gaps -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). EMBL; X70529; X70529. EMBL; Z36134; Z36134. PIR; S32966; S32966. HYPOTHETICAL PROTEIN; TRANSMEMBRANE. :: 01-0CT-1994 (REL. 30, CREATED) 01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE) 01-0CT-1994 (REL. 30, LAST ANNOTATION UPDATE) HYPOTHETICAL 36.0 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION. Length 517; 9; Mismatches 10; Indels EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES Score 86; DB 8; L Pred. No. 3.41e-01; STRAIN-S288C; MEDLINE; 93220397. DOIGNON F., BITEAU N., CROUZET M., AIGLE M.; YEAST 9:189-199(1993). 320 AA. 475 igilgafvlllgllaflqyrrlrkgyaplmetgl 508 30 IGILTVILGVLLIGGWYCRR-RNGYRALMDKSL 62 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). 320 AA; 35986 MW; 532496 CN; POTENTIAL. POTENTIAL. POTENTIAL Query Match 9.7%; Best Local Similarity 41.2%; 14; Conservative STANDARD; YBR265W OR YBR1734. SEQUENCE FROM N.A. YB9K\_YEAST P38342; TRANSMEM TRANSMEM SEQUENCE TRANSMEM 9 Matches RESULT g ð 

Query Match 9.6%; Score 85; DB 9; Length 320; Best Local Similarity 41.7%; Pred. No. 4.82e-01;

3

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; Gaps ACTIVE TRANSPORT OF NUTRIENTS BY H+- SYMPORT. THE RESULTING EXTERNAL ACIDIFICATION AND/OR INTERNAL ALKINIZATION MAY MEDIATE HYDROGEN ION PUMP. THE PROTON GRADIENT IT GENERATES DRIVES THE PROSITE; PS00154; ATPASE E1 E2. HYDROLASE; HYDROGEN ION TRANSPORT; TRANSMEMBRANE; PHOSPHORYLATION; -!- FUNCTION: THE PLASMA MEMBRANE ATPASE OF PLANTS AND FUNCT IS A -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
-!- THERE ARE TWO PLASMA MEMBRANE ATPASES IN YEAST. THIS IS THE -!- PTM: PHOSPHORYLATED ON MULTIPLE SER AND THR RESIDUES. -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY 5; Indels EXTRACELLULAR (POTENTIAL) 01-NOV-1995 (REL. 32, IAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, IAST ANNOTATION UPDATE) PLASMA MEMBRANE ATPASE 1 (EC 3.6.1.35) (PROTON PUMP). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. 4; EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES. SERRANO R., KIELLAND-BRANDT M.C., FINK G.R.; NATURE 319:689-693(1986). 918 AA. 8; Mismatches ATP-BINDING; MULTIGENE FAMILY; GLYCOPROTEIN. 1 (POTENTIAL). 2 (POTENTIAL). 3 (POTENTIAL). SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). PRT; fgvlsnilvvpfymvgcswyirkw 310 :|:|: || | : ::|| || |:: 30 IGILTVILGV-LLLIGC-WYCRRR 51 13-AUG-1987 (REL. 05, CREATED) Conservative STANDARD; PIR; A25823; PXBY1P. LISTA; SC00832; PMA1. SGD; L0001449; PMA1. EMBL; X03534; X03534. GROWTH RESPONSES (E1-E2 ATPASES) SEQUENCE FROM N.A. MEDLINE; 86146844. MAJOR ISOFORM 116 137 137 141 161 292 334 325 348 720 739 755 775 10; ATH1 YEAST **FRANSMEM TRANSMEM** FRANSMEM P05030; DOMAIN DOMAIN DOMAIN 287 Matches 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013091 2013001 2013001 2013001 2013001 2013001 2013001 2013001 20130001 20130001 20130001 20130000000 셤 ð

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MARTIN L.H., CALABI F., LEFEBVRE F.-A., BILSLAND C.A.G., MILSTEIN C., PROC. NATL. ACAD. SCI. U.S.A. 84:9189-9193(1987). -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN. -!- TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN Gaps T-CELL LEUKEMIAS, AND IN VARIOUS OTHER TISSUES.
-!- SIMILARITY: TO OTHER CD1 ANTIGENS, AND TO MHC CLASS I ANTIGENS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. 01-Ja"-1988 (REL. 06, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
T-CELL SURFACE GLYCOPROTEIN CDIA PRECURSOR (CDIA ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTAI THYMOCYTE ANTIGEN). GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE; IMMUNOGLOBULIN FOLD; T-CELL; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 4; Score 85; DB 1; Length 918; Pred. No. 4.82e-01; 11; Mismatches 14; Indels 282 gggh-ftevlngigiillvlviatlllvwtacfy-rtngivril 323 -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. 327 AA. CDIA ANTIGEN PRT; ARUFFO A., SEED B.; J. IMMUNOL. 143:1723-1730(1989). SEQUENCE OF 99-327 FROM N.A. Query Match 9.6%; Best Local Similarity 34.1%; PIR; A45801; A45801. HSSP; P01842; 1DLH. MIM; 188370; 11TH EDITION. Conservative NATURE 323:540-543(1986). STANDARD; -!- FUNCTION: NOT KNOWN. CALABI F., MILSTEIN C.; EMBL; M22080; M22080. EMBL; M22163; M22163. EMBL; M22164; M22164. EMBL; M22165; M22165. EMBL; M22166; M22166. 16 327 108 201 EMBL; M28825; M28825. EMBL; X04450; X04450. M22167 HOMO SAPIENS (HUMAN) PIR; A02242; HLHUCD. [2] SEQUENCE FROM N.A. MEDLINE; 89341413. PIR; A39957; A39957 EUTHERIA; PRIMATES SEQUENCE FROM N.A. MEDLINE; 87014824. MEDLINE; 88097453 MULTIGENE FAMILY. 17 17 109 TISSUE=T-CELL; EMBL; M22167; CD1A HUMAN CHAIN DOMAIN DOMAIN SIGNAL Matches 3 RESULT 염 à

EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2.

CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (PROBABLE).

DOMAIN MOD RES BINDING

CARBOHYD

DOMAIN DOMAIN

TRANSMEM

DOMAIN

ATP (BY SIMILARITY).

POTENTIAL.

25 POLY-SER. 78 ASP/GLU-RICH (ACIDIC). 99619 MW; 4420147 CN;

SEQUENCE

7 (POTENTIAL). EXTRACELLULAR (POTENTIAL)

8 (POTENTIAL)

857

DOMAIN TRANSMEM

DOMAIN TRANSMEM

CYTOPLASMIC (POTENTIAL).

(POTENTIAL)

5 (POTENTIAL). EXTRACELLULAR (POTENTIAL)

CYTOPLASMIC (POTENTIAL).

DOMAIN TRANSMEM DOMAIN TRANSMEM

4 . (POTENTIAL) .

EXTRACELLULAR (POTENTIAL)

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Gaps

1;

<del></del>		3;			
-2.sp	R ALPHA-3. Y. Y. EF. 1).	Length 327; ; 4; Indels 3; Gaps		99 MOUSE STANDARD; PRT; 306 AA.  109; 109; 109; 1094 (REL. 28, CREATED) 108-1994 (REL. 28, LAST SEQUENCE UPDATE) 108-1995 (REL. 32, LAST ANNOTATION UPDATE) 108-1995 (REL. 32, LAST ANNOTATION UPDATE) 108 BJ.  MCHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1) 108 BJ.  MUSCULUS (MOUSE).  MENOTAL METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  ERIA; RODENTIA.  ERIA; RODENTIA.  E. M., FINGEROTH J.D., GRIBBEN J.G., NADLER L.M.;  E. M., FINGEROTH J.D., GRIBBEN J.G., NADLER L.M.;  E. M., FINGEROTH J.D., GRIBBEN J.G., NADLER L.M.;  AKUMAR A., WHITE P.C., DUPONT B.;  NOGENETICS 38:292-295(1993).  INTE; 93307189.  INTE; 93307180  INTERCETOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LIMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.  SUBCELLIJUAR LOCATION: TYPE I MEMBRANE PROTEIN.  DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-ACTIVATION. PROTEIN WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION. PROPULITED MONOCYTES AND NONCIRCULATING B-CELL MALIGNANCIES.  SIMILARIATY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAIN.  17 12502 STALLS.  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505  11 12505	
US-08-231-565A-2.rsp	EXTRACELLULAR ALPHA-3 POTENTIAL. CYTOPLASMIC (POTENTIA. BY SIMILARITY. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. I -> T (IN REF. 1). W -> C (IN REF. 1). MW; 559220 CN;	Score 84; DB 2; Pred. No. 6.78e-01 7; Mismatches	wf-rkr 324  :  :  WYCRRR 51	ERTEBRE ERTEBRE CD80 CD80 CD0, EN J.G EN J.G ELL PR E BIND I MEMB SED DN FROM FROM FROM FROM FROM FROM FROM FROM	
	2 294 2 321 2 321 9 183 7 37 6 66 0 60 145 5 145 8 68	9.4%; arity 48.1%; Conservative	svgfiilavivplllliglalwf-rkr :  :   :  : :       :  :  AAGIGILTVILGVLLIG-C-WYCRRR	9 10 MOUSE STANDARD; 1609; 17:E8-1994 (REL. 28, LAST SEQ 1804-1995 (REL. 28, LAST SEQ 1804-1995 (REL. 32, LAST SAN 2MPHOCYTE ACTIVATION ANTIGE 11GEN) (BT). 10 MS DT. 11GEN) (BT). 11GEN) (	L12585. L12587.
Aug 27 07:55	DOMAIN 202 DOMAIN 302 DOMAIN 322 DISULFID 119 CARBOHYD 60 CARBOHYD 74 CARBOHYD 145 CONFLICT 30 CONFLICT 36 SEQUENCE 327 1	Query Match Best Local Similarity Matches 13; Conser	299 svgfiilavivplllliglalwf-rkr :  :   :  :  :        :  :  27 AAGIGILTVILGVLLIG-C-WYCRRR	DD80 0006 0006 0006 0005 0005 0005 0005 00	EMBL; L12585; EMBL; L12587; EMBL: 112599.
Aug	2111111111	A Be	Db Qy	RESULT 10 D D T T T D D D T T D D D D D D D D D	<b>* * *</b>

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MIYAJIMA A.;
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                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                          J. BIOL. CHEM. 265:4064-4071 (1990).
-!- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE INTERFERON-CAMMA DIMER.
                                                                                                                                       -!- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERFERON-GAMMA RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR; TRANSHEMBRANE; GLYCOPROTEIN; SIGNAL; PHOSPHORYLATION; IMMUNOGLOBULIN FOLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAYASHIDA K., KITAMURA T., GORMAN D.M., ARAI K., YOKOTA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.2%; Score 82; DB 4; Length 477; Best Local Similarity 36.1%; Pred. No. 1.33e+00; Matches 13; Conservative 13; Mismatches 6; Indels
                     COFANO F., MOORE S.K., TANAKA S., YUHKI N., LANDOLFO S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                      -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 vapltvítvvilvíaywy-tkknsíkrksimlpksl 294
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01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE) CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                               TWO IG-LIKE DOMAINS.
                                                                                                                                                                                                                                    EMBL; M28995; M28995.
EMBL; M26711; M26711.
EMBL; M28733; M28233.
EMBL; J05265; J05265.
EMBL; J05265; J05265.
PIR; A34368; A34368.
PIR; A34508; A34508.
PIR; A35468; A35468.
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208
243
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   MEDLINE; 90154099
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CYRB HUMAN
P32927;
                                           APPELLA E.;
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DISULFID
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Aug 27 07:55 US-08-231-565A-2.rsp

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4;
                  -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5 AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                         POTENTIAL. CYTOKINE RECEPTOR COMMON BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). EMBL; X79489; X79489. EMBL; Z35867; Z35867. PIR; S45389; S45389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                 CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
--- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
--- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
--- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 82; DB 2; Length 897;
Pred. No. 1.33e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                  TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBERMAIER B., GASSENHUBER J., PIRAVANDI E., DOMDEY H.;
                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 gfgdsevspltiedpkhvcdppsgpdttpaasdlptegppsp 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GFDHRD-SKVSLQE-KN-CEPVV-PNAPPAYEKLSAEQSPPP 115
                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-III.
PROC, NATL. ACAD. SCI. U.S.A. 87:9655-9659(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YBL106C OR YBL0806.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994 (REL. 30, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 111.7 KD PROTEIN IN PKC1 5'REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1010 AA; 111678 MW; 5433252 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                               PIR; A39255; A39255.
MIM; 138981; 11TH EDITION.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2.
                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97323 MW;
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Best Local Similarity 33.3%;
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                                                                                                                                                                            EMBL; M59941; M59941.
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Aug 27 07:55

ö INFORMATION AND VOR VISCAL LEARNING.

-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-! SIMILARIY'S BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

-! SIMILARIY'S 171234.

R PIR; \$44275; \$44275.

R FUNDES, FGROUDIS82, DOPR.

R FLYBASE, FGROUDIS82, DOPR.

R PROSITE; PROOFEIN RECEPTOR.

R PROSITE; PROOFEIN RECEPTOR.

R PROSITE; PROOFEIN RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;

PHOSPHORYLATION; PALMITATE; SIGNAL. Gaps .; 0 -!- FUNCTION: MIGHT BE INVOLVED IN THE PROCESSING OF VISUAL Score 82; DB 9; Length 1010; Pred. No. 1.33e+00; 9; Mismatches 18; Indels EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). 759 dthalfkypiatsglsfipiidgkgerklstimivlling 798 EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA. |:| |: || | |: || | |: || || || 5 DAHFIYCYPKKGHGHSYTTAEEAAGIGILIVILGVLLLIG 44 DOPAMINE RECEPTOR. 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) 511 AA (POTENTIAL). (POTENTIAL) . (POTENTIAL) . (POTENTIAL) 4 (POTENTIAL) (POTENTIAL) POTENTIAL. DOPAMINE RECEPTOR PRECURSOR (D-DOP1). DROSOPHILA MELANOGASTER (FRUIT FLY) GOTZES F., BALFANZ S., BAUMANN A.; RECEPT. CHANNELS 2:131-141(1994). STRAIN=BERLIN; TISSUE=HEAD; Best Local Similarity 32.5%; Conservative STANDARD; 331 384 420 427 450 SEQUENCE FROM N.A. 20 20 143 170 170 207 217 240 259 285 307 330 332 393 421 428 451 LT 13 DOPR\_DROME P41596; DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN Query Match TRANSMEM RANSMEM SIGNAL DOMAIN DOMAIN DOMAIN CHAIN Matches 음 ð

ä Gaps 3 Score 81; DB 3; Length 511; Pred. No. 1.86e+00; 7; Indels US-08-231-565A-2.rsp 9; Mismatches Query Match 9.1%; Best Local Similarity 36.7%; Aug 27 07:55 Matches

셤 δ

11; Conservative

CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT, TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND FACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE. OF METHYLATION, ATTRACTANTS INCREASE THE LEVEL OF METHYLATION WHILE REPELLENTS DECREASE THE LEVEL OF METHYLATION, THE METHYL GROUPS ARE ADDED BY THE METHYLTRANSFERASE CHER AND REMOVED BY THE FUNCTION: CHEMOTACTIC-SIGNAL TRANDUCERS RESPOND TO CHANGES IN THE -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE. -!- SIMILARITY: TO THE OTHER BACTERIAL CHEMOTAXIS SENSORY TRANSDUCERS. POTENTIAL. CYTOPLASMIC (POTENTIAL). THE 3 ARG MAY FORM A POSITIVELY CHARGED AMINO AND DICARBOXYLIC ACIDS. TAR MEDIATES TAXIS AWAY FROM THE REPELLENTS COBALT AND NICKEL. UNLIKE E.COLI TAR IT DOES NOT -!- FUNCTION: RECEPTOR FOR THE ATTRACTANT L-ASPARTATE AND RELATED PROSITE; PS00538; CHEMOTAXIS TRANSDUCER. CHEMOTAXIS; TRANSDUCER; TRANSMEMBRANE; METHYLATION; PERIPLASMIC; X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 36-180. YEH J.I., BIEMANN H.-P., PANDIT J., KOSHLAND D.E., KIM S.-H.; J. BIOL. CHEM. 268:9787-9792(1993). 12-JUL-1986 (REL. 01, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) METHYL-ACCEPTING CHEMOTAXIS PROTEIN II (MCP-II) (ASPARTATE POTENTIAL.

TAR PROTEIN.

PERIPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) STOCK A.; THESIS (1986), UNIVERSITY OF BERKELEY, U.S.A. 553 AA. [2] REVISIONS TO 236 AND INSERTION OF ALA-498. PRT; RUSSO A.F., KOSHLAND D.E. JR.; SCIENCE 220:1016-1020(1983). OUTER MEMBRANE; 3D-STRUCTURE. MEDIATES MALTOSE TAXIS. STANDARD; METHYLESTERASE CHEB 33 552 190 215 552 73 SALMONELLA TYPHIMURIUM. CHEMORECEPTOR PROTEIN) STYGENE; SG10387; TAR PDB; 1WAS; 15-JAN-95. PDB; 1WAT; 15-JAN-95. EMBL; J01809; J01809 PIR; A03441; QREBDT. [1] SEQUENCE FROM N.A. MEDLINE; 83197387 STRAIN=LT2; SALTY DOMAIN TRANSMEM **TRANSMEM** DOMAIN DOMAIN DOMAIN CHAIN MCP2\_S P02941  $\overline{\Xi}$ 

CYTOPLASMIC (POTENTIAL).

POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL

CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD

POTENTIAL.

(POTENTIAL)

**TRANSMEM** 

DOMAIN

(POTENTIAL) .

168 PALMITATE (POTENTIAL) 169 PALMITATE (POTENTIAL) 55997 MM; 1403905 CN;

511 AA;

SEQUENCE

BY SIMILARITY

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1;
                                                                                                                                                                    Gaps
                                 POCKET, WHICH BINDS THE ALPHA-CARBOXYL GROUP OF THE ATTRACTANT AA. DEAMIDATION AND METHYLATION. METHYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                 A BASRAI M.A., LUBKOWITZ M.A., PERRY J.R., MILLER D., KRAINER E.,
BASRAI M.A., LUBKOWITZ M.A., PERRY J.R., MILLER D., KRAINER E.,
A NAIDER F.R., BECKER J.M.;
L MICROBIOLOGY 141:147-1156 (1995).
C -!- FUNCTION: UPTAKE OF SMALL PEPTIDE.
C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
C -!- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
R PROSITE; PSO1023; PTR2 1.
R PROSITE; PSO1023; PTR2 1.
R PROSITE; PSO1023; PTR2 1.
W PROSITE; PSO1023; PTR2 1.
W PROSITE; PSO1023; PTR2 1.
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                                                                                    DEAMIDATION AND METHYLATION.
                                                                                                                                       Query Match 9.1%; Score 81; DB 5; Length 553; Best Local Similarity 40.9%; Pred. No. 1.86e+00;
                                                                                                                                                                  4; Indels
 US-08-231-565A-2.rsp
                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI)
                                                                                                                                                                                                                                                                       PTR2 CANAL STANDARD; PRT; 623 AA. P46030; 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                   8; Mismatches
                                                                                                  191 METHYLATION.
59511 MW; 1383542 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.1%;
Best Local Similarity 39.1%;
Matches 9; Conservative
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553 AA;
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623 AA;
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Gaps

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_tpn n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols

Run on:

Tue Aug 27 18:41:56 1996; MasPar time 34.18 Seconds 736.520 Million cell updates/sec

Tabular output not generated.

>US-08-231-565A-2 (1-118) from US08231565A.pep 1420 Perfect Score: Description:

1 ATGCCNMGNGARGAYGCNCA......SNCCNCCNCCNTAYWSNCCN 354 TACGGNKCNCTYCTRCGNGT..........nngGNGGNGANATRS#NGGN

N.A. Sequence:

Comp:

TABLE bktranslate2 Scoring table:

Gap 30

91712 seqs, 35561689 bases x 2 Searched:

Dbase 0; Query 0

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STD

Nmatch

Minimum Match 0% Post-processing:

Listing first 45 summaries

Database:

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14:part14 15:part15 16:part16 17:part17 n-geneseq23

Mean 48.264; Variance 223.558; scale 0.216

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ered. No.	35e-108	.83e-107	3.77e-103	.85e-24	.55e-02	,31e-01	47e+00	.04e+00
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11	T02714	976370	T11550	T11549	N10053	N60354	020927	Q63952
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ບ	14	123	œ	~	657	7	043519	Degenerate FMN reduct	2.24e+01
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υ	16	122		9	720	6	053372	Sequence encoding glu	2.58e + 01
	17	122		9	2158	m	014624	PATDPD in	2.58e+01
	18	122		9	3186	m	014631	Plasmid pTM72 insert	2.58e+01
	19	121		S	315	œ	061284	Human brain Expressed	2.98e+01
o	20	121		2	174	ო	022981	Gelonin toxin DNA.	2.98e+01
υ	21	121	•	S	5437	7	013369	Fusaric acid resistan	2.98e+01
	22	121	•	5 1	34525	-	004525	Total base sequence o	2.98e+01
	23	118		٣	501	ო	N50025	se encoding	4.55e+01
	24	116	œ	2	1269	12	094256	CAIR-1 cDNA clone 21D	6.02e+01
U	52	117	•	7	1764	œ	046070	Sequence of potato po	5.23e+01
υ	56	117	•	7	1858	10	056131	Potato polyphenol oxi	5.23e+01
U	27	117	•	7	1900	-	N70813	Aspergillus nidulans	5.23e+01
	88	117	•	2	2107	m	021182	Encodes B lymphocyte-	5.23e+01
	59	117	•	7	3190	9	038746	CD22-beta gene.	5.23e+01
ပ	30	117	•	2	11561	16	092323	Aspergillus terreus t	5.23e+01
ပ	31	115	œ	_	501	m	N50026	Sequence encoding new	6.91e+01
v	32	115	-	_	501	ო	N50030	Sequence encoding new	6.91e+01
υ	33	115		_	501	က	N50032	Sequence encoding new	6.91e+01
υ	34	114		0	204	-	N81164	Base substituted E.co	7.94e+01
	35	113	-	0	420	14	088233	Bovine aFGF synthetic	9.11e+01
ບ	36	114	<u>~</u>	0	1065	11	094335	Degenerate Alteromona	7.94e+01
	31	112	•	6	501	٣	N50027	Sequence encoding new	1.04e+02
บ	38	112	-	6	2054	4	024216	Squalene synthase.	1.04e+02
	39	112	-	6	3731	S	032631	Porcine PAM-8.	1.04e+02
	40	112	7	6	3746	-	N90693	Bovine peptidyl-glyci	1.04e+02
	41	112	7	6	6751	Ξ	079727	Mouse L5/3 tumour sup	1.04e+02
	42	111	-	œ	453	15	089545	Orchid bibenzyl synth	1.20e+02
	43	111	۲.	œ	1482	-		(1	1.20e+02
	44	111	7	œ	1517	-	45	ine neraminic	1.20e+02
	45	110	7.	_	4258	m	Q22439	DNA of hgEco-1, encod	1.37e+02

## ALIGNMENTS

MART-1; melanoma antigen recognised by T-cells; melanoma; metastatic melanoma; tumour-associated antigen; immunogen; diagnosis; prognosis; prophylaxis; therapy; vaccine; ds. Location/Qualifiers 54..410 T02714 standard; cDNA; 1559 BP. 20-APR-1996 (first entry) MART-1 melanoma antigen. Mammalian. RESULT 

(USSH ) US SEC DEPT HEALTH. Rosenberg SA; 02-NOV-1995, 21-APR-1995, U05063, 22-APR-1994, US-231565, 05-APR-1995, US-417174. /\*tag= a WO9529193-A2.

DNA encoding melanoma antigens recognised by T-lymphocytes - also vectors, host cells and antibodies, used to detect, treat and Kawakami Y, Rosenbe WPI; 95-382963/49. P-PSDB; R84212.

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ö atgccaagagaagatgctcacttcatctatggttacccaagaaggggcacggcact 113 234 agtetteatgttggeaeteaatgtgeettaacaagaagatgeeeacaagaaggtttgat 293 294 catogggacagcaaagtgtotottcaagagaaaaactgtgaacctgtggttoccaatgot 353 300 The nucleic acid encodes a melanoma antigen (MART-1) which is recognized by T-lymphocytes. It is used for recombinant protein production, preferably using a baculo virus vector for expression insect cell cultures. MART-1 protein is a source of immunogenic peptides (see R84196 for peptide M9-2) which are optionally modified (see R84783-R84800) and used in medicaments for the treatment or prevention (by immunization) of melanoma. Antibodies against MART-1 114 tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 173 61 TAYACNACNGCNGARGARGCNGCNGGNATHGGNATHYTNACNGTNATHYTNGGNGTNYTN 120 174 ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaa 233 1 ATCCCHMCHCARGAYGCNCAYTTYATHTAYGGNTAYCCHAARAARGGNCAYGGNCAYWSN 60 Gaps Tumour rejection antigen; precursor; HLA-A2 molecule; tyrosinase; isolation; melanoma; cell line; LB-39-MEL; diagnosis; vaccine; indicative of a disease state (melanoma or metastatic melanoma). 354 coacctgcttatgagaaactctctgcagaacagtcaccaccaccttattcacc 406 ö and its immunogenic peptides may be used in the detection and isolation of MART-1 from a sample, the detection of which is Length 1559; 81; Mismatches 65; Indels Score 1392; DB 17; Pred. No. 1.35e-108; Tumour rejection antigen precursor cDNA. 330 C; Claim 2; Page 115-116; 184pp; English. Location/Qualifiers immunise animal against melanoma LUDWIG INST CANCER RES. 470 A; 98.0%; 58.6%; Q76370 standard; cDNA; 354 26-MAY-1995 (first entry) 207; Conservative /codon= seq:CGA, aa:Pro /codon= seq:GAC, aa:His 09-MAR-1994; U02487. 18-MAR-1993; US-032978. misc difference 49..51 Key Locat misc\_difference 4..6 1559 BP; Local Similarity Homo sapiens. therapy; ss. 29-SEP-1994 /\*tag= a /\*tag= b Sequence Query Match (LUDM-) 076370; Matches 54 301 RESULT DI COLO 셤 g 셤 g 쇰 쇰 ð à ð δ δ ò

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for therapy of disorders characterised by the expression of the tumour processed to a tumour rejection antigen presented by HLA-A2 molecules. 61 TAYACNACNGARGARGARGANGCNGGNATHGTNACNGTNATHYTNGGNGTNYTN 120 181 agtetteatgttggeacteaatgtgeettaacaagaagatgeecacaagaagggtttgat 240 300 61 tacaccacggetgaagaggeegetgggateggeateetgacagtgateetgggagtetta 120 121 ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaa 180 121 YINYINATHGGNIGYIGGIAYIGYMGNMGNMGNAAYGGNIAYMGNGCNYINAIGGAYAAR 180 9 tumour rejection antigen may be used for diagnosis or in vaccines or 1 atgcgaagagaagatgctcacttcatctatggttaccccaagaagggggacggccactct 60 Gaps used for developing prods. for diagnosis or treatment of expression This sequence encodes the tumour rejection antigen precursor which catcgggacagcaaagtgtctcttcaagagaaaaactgtgaacctgtggttcccaatgct Nucleic acid coding for a tumour rejection antigen precursor - is Tumour rejection antigen precursor; TRAP; TRA; melanoma; cancer; tumour; treatment; detection; vaccine; HLA-A2; adoptive transfer; T cell; T lymphocyte; human leukocyte antigen; ss. This sequence was isolated from the melanoma cell line, LB-39-MEL. ocacctgcttatgagaaactctctgcagaacagtcaccaccaccttattcacc 353 CCNCCNGCNTAYGARAARYTNWSNGCNGARCARWSNCCNCCNCCNTAYWSNCC 353 0; Length 354; The tumour rejection antigen is not related to tyrosinase. Indels 낊 rejection antigen precursor, particularly melanoma Pumour rejection antigen precursor coding sequence De PLAEN 81; Mismatches 67; 96.6%; Score 1372; DB 12; 58.1%; Pred. No. 8.83e-107; 86 G; De Plaen E, (LUDM-) LUDWIG INST CANCER RES. Boon-falleur T, Brichard V, Coulie P, Traversari C, Van PEL A, Wolfel T; 86 C; related disorders, partic. melanoma Claim 5; Page 14; 26pp; English. T11550 standard; cDNA; 760 BP Brichard V, 99 A; Best Local Similarity 58.18; Matches 205; Conservative 18-APR-1996 (first entry) 27-JUN-1995; U08153. 08-JUL-1994; US-272351. 10-JAN-1995; US-370319. 354 BP; WPI; 94-316544/39. P-PSDB; R63158. Boon-Falleur T, E Van Pel A, Wolfel WPI; 96-097390/10. Homo sapiens. WO9601557-A1. 25-JAN-1996. Sequence Query Match T11550; 301 241 301 염 임 음 셤 ð 임 셤 ð ð δλ δ ð

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ö 61 TAYACNACNGCNGARGARGCNGCNGCNGTHGCNATHYTNACNGTNATHYTNGGNGTNYTN 120 161 atgccaagagaagatgctcacttcatctatggttaccccaagaaggggcacggccactct 220 221 tacaccacggctgaacaggccgctgggatcggcatcctgacagtgatcctgggagtctta 280 341 agtetteatgttggeaeteaatgtgeettaaeaagaagatgeeeaeaagaaggtttgat 400 catcgggacagcaaagtgtctcttcaagagaaaaactgtgaacctgtggttcccaatgct 460 is used to generate cytotoxic T lymphocytes for treating cancer (esp. transfer or generated, or they can be generated in vivo by using a vector containing the appropriate gene or using TRA or TRAP together with an adjuvant that facilitates entry into HLA-A2 presenting cells. Diagnostic methods involving the detection of expression of TRAP Gaps melanoma). It can also be used to raise specific antibodies, and when complexed with HLA-A2, it can be used to prduce vaccines. adoptive transfer; processed to antigen presented by HLA-A2, useful for treating or Tumour rejection antigen precursor; TRAP; melanoma; cancer; The tumour rejection antigen precursor (TRAP) is processed to a 461 gcaggtgcttatgagaaactctctgcagaacagtcaggaccaccttattcacc 513 tumour rejection antigen (TRA) presented by HLA-A2 molecules. ö Cytotoxic I lymphocytes so generated can be used in adoptive Score 1332; DB 17; Length 760; Pred. No. 3.77e-103; 180 T; 81; Mismatches 71; Indels Genomic DNA encoding a tumour rejection antigen precursor Tumour rejection antigen precursor coding sequence. /\*tag= b /note= "This region is 4.7-5.3 kilobases in length 167 G; tumour; treatment; detection; vaccine; HLA-A2; cell; T lymphocyte; human leukocyte antigen; can be used in the detection of cancers. Sequence 760 BP; 247 A; 166 C; Claim 4; Page 22-23; 41pp; English. Location/Qualifiers T11549 standard; DNA; 13585 BP Query Match
Best Local Similarity 56.9%; 18-APR-1996 (first entry) 201; Conservative diagnosing melanoma misc feature Homo sapiens. Query Match T11549; Matches 401 g 召 g g 

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11517 gataaaagtetteatgttggeaneteaatgtgeettaacaagaagatgeecaeaagaagg 11576 175 GAYAARWSNYTNCAYGTNGGNA-CNCARTGYGCNYTNACNMGNMGNTGYCCNCARGARGG 233 vector containing the appropriate gene or using TRA or TRAP together 11577 gtttgatcatcgggacagcaaagtgtctttcaagagaaaaactgtgaacctgtggt 11633 cells Gaps transfer or generated, or they can be generated in vivo by using a is used to generate cytotoxic T lymphocytes for treating cancer (emelanoma). It can also be used to raise specific antibodies, and ö Diagnostic methods involving the detection of expression of TRAP can be used in the detection of cancers. 3894 T; The tumour rejection antigen precursor (TRAP) is processed to a tumour rejection antigen (TRA) presented by HLA-A2 molecules. I 1; with an adjuvant that facilitates entry into HLA-A2 presenting when complexed with HLA-A2, it can be used to prduce vaccines. processed to antigen presented by HLA-A2, useful for treating Score 443; DB 17; Length 13585; Pred. No. 2.85e-24; Cytotoxic T lymphocytes so generated can be used in adoptive Genomic DNA encoding a tumour rejection antigen precursor 31; Mismatches 19; Indels 2968 G; De PLAEN E; 2859 C; Coulie P, (LUDW-) LUDWIG INST CANCER RES.
Boon-falleur T, Brichard V, Coulie
Traversari C, Van PEL A, Wolfel T; Claim 3; Page 18-22; 41pp; English. /\*tag= c /note= "Unidentified nucleotide." 3827 A; Query Match Best Local Similarity 56.4%; 66; Conservative 08-JUL-1994; US-272351. 10-JAN-1995; US-370319. 13585 BP; 27-JUN-1995; U08153. diagnosing melanoma WPI; 96-097390/10. W09601557-A1. · misc feature 25-JAN-1996, Sequence Query Match Matches 쇰 임 ð ð

Generic coding sequence for human preproinsulin. Hormone; insulin; diabetes; ss. Location/Qualifiers N10053 standard; DNA; 416 BP. 17-0CT-1992 (first entry) 17..19Leu" 38..40 29..31ren\_ "encodes Leu" "encodes "encodes "encodes Homo sapiens N10053; /\*tag= /\*tag= /note= /\*tag= unsure /note= unsure /\*tag= /\*tag= 'note= nsure /note= unsure unsure 

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but the sequence of this region has not been deduced."

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= "encodes Leu"
275..277
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266..268
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176..178
                                                                                                                                                                                                                        Leu"
212..214
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254..256
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131..133
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239..241
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263..265
                                                                                                                                                      "encodes Leu"
146..148
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insure 191..193
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nnsure 236..238
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insure 113..115
                                                                                                                    "encodes Leu"
125..127
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unsure 173..175
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                                      50..52
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277 ARTIYITYTCYTGNARNWSNACYTINWSRTCNCKRTGRTCRAANCCYTCYTGNGGRCANC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 KNCKNGTNARNGCRCAYTGNGTNCCNACRTGNARNWSYTTRTCCATNARNGCNCKRTANC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 mgnytnytnccnytnytngcnytnytngcnytntggggnccngayccngcngcngcntty 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   sequences able to code for the human preproinsulin amino acid sequence. The features table indicates where Leu, Ser or Arg codons are intended. These 3 amino acids cannot readily be specified by a single generic codon, hence the need for clarification. For each of
                                                                                                                                                                                                                                                                                                                                                                                   This coding sequence is a generic coding sequence which covers DNA
                                                                                                                                                                                                                                                                                                                                      DNA transfer vectors contg. codes for human insulin precursors - used to transform microorganisms for insulin prodn. Claim 4; Page 33; 50pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intended, respectively: YTR and CTY (= Leu), MGR and CGY (= Arg) and TCN and AGY (= Ser). Transfer vectors containing DNA whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Mismatches 102; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 mgngcnttyttytayacnccnaaracnmgnmgngargcngargayytncar 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 159; DB 4; Length 416; Pred. No. 9.55e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence corresponds to this generic sequence are claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desulphatohirudin; antibodies; thrombin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 C;
                                                                                                                                                                                                                                             31-DEC-1980,
11-SEP-1980, 885196,
12-SEP-1979, US-075192,
(REGC ) UNIV OF CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N60354 standard; DNA; 231 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%;
                                                                                                                                                                                                                 'product= human_preinsulin
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                                           311..313
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EP-168342-A.
15-JAN-1986.
10-JUN-1985; 810268.
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                                                                                                                      'note= "encodes Leu"
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P-PSDB; P10053.
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and the digest product run on a standard agarose gel. The isolated DNA fragment was inserted into the pUC18 cloning vector using T4 DNA ligase. The sequence is a repetitive element present 40 or more times in the L. hardjo-bovis genome. Therefore this element provides

The sequence was obtd. by shearing L. hardjo-bovis total genomic DNA to 5 kbp fragments. These were denatured to single strands and allowed to reanneal slowly to form fragments contg. the double stranded sequence of 1.4 kbp flanked by shorter regions of single

stranded DNA. These regions were digested away using S1 nuclease

Identifying L. hardjo-bovis by hybridisation probing of DNA - is useful for detecting presence of Leptospira organisms in body

(UKAG-) UK MIN AGRIC FISH. 27-JUL-1990; GB-016516. 26-JUL-1991; GB-016211. 29-JAN-1992. 26-JUL-1991; 016211.

WPI; 92-034842/05.

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Claim 11; Page 14; 21pp; English.

infection; plasmids; multiple repetitive elements; genetic probing;

Leptospira hardjo-bovis probe. 08-MAY-1992 (first entry)

Q20927 standard; DNA; 1467 BP.

Leptospira hardjo-bovis, strain CVL B215.

hybridisation; ds GB2246354-A.

27 18:30 US-08	US-08-231-565A-2 mg 9
14-JW-1984; CH-288284. (CIBA ) CIBA GEIGY AG. Liersch M. Rink H. Marki W. Grutter MG, Meyhack B. WPI; 86-015589/03.	er MG, Meyhack B.
Dr. Sequences coding for hirudin and derivs and expression vectors, transformed cells, monoclonal antibodies and hybridomas, useful as thrombin inhibitor.	and derivs. — and expression lonal antibodies and hybridomas,
Disclosure; Page 8; 123pp; German. The sequence pref. comprises an EcoRI restriction enzyme site at t) 5'-end and a BamHI restriction enzyme site at the 3'-end. See N60355 for the preferred sequence. The sequence may be introduced	coll restriction enzyme site at the yyme site at the 3'-end. See . The sequence may be introduced
into a vector for the transformation of hosts, e.g. E. coli. The hirudin can thus be prepared on a large scale. The product and its derivs. are thrombin inhibitors, useful in anticoagulant therapy, esp. when injected at doses of 0.01-0.05 mg/kg. Sequence 231 BP; 43 A; 16 C; 41 G; 22 T;	ion of hosts, e.g. E. coli. The large scale. The product and its useful in anticoagulant therapy, 01-0.05 mg/kg.
rry Match 11.1%; Score the Local Similarity 10.7%; Pred. ches 17; Conservative 58; M	Score 157; DB 2; Length 231; Pred. No. 1.31e-01; 58; Mismatches 83; Indels 1; Gaps 1;
59 gyytntgygamggnwsnaaygtntgyggn 	59 gyytntgygamggnwsnaaygtntgyggncamggnaayaamtgyatnytnggnwsngayg 118 ::::   : : :   : : : : : :: : : : : : :
119 gngamaamaaycamtgygtnacnggngam : ::  :: :  216 NCKNGTNARNGCRCAYTGNGTNCCNACRT	119 gngamaamaaycamtgygtnacnggngamggnacnccnaamcorcamwsncayaaygayg 178 : : : :   : : :   : : : : : : : : : :
179 gngayttygamgama-tnccngamgamtayytncamtmk 216 : :: :: :: ::           : ::     ::         ::             ::	yytncamtmk 216  :  : :: ATMARNARNAR 1.18

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Q10572 standard; DNA; 1047 BP.

09-APR-1991

US-08-231-565A-2 mg

ö ö 2764 gtccccactcgtacttcgatactttgtattttaaagtggagttgcgcgacacaaacggtg 2823 2764 gtccccactcgtacttcgatactttgtattttaaagtggagttgcggcgacacaaacggtg 2823 221 GYCCNCARGARGGNTTYGAYCAYMGNGAYWSNAARGTNWSNYTNCARGARAARAAYTGYG 280 221 GYCCNCARGARGGNTTYGAYCAYMGNGAYWSNAARGTNWSNYTNCARGARAARAYTGYG 280 Gaps Viral enhancing factor from a granulosis virus. VEF; baculovirus; pesticides; insecticide; peritrophic membrane; ss. Trichoplusia ni granulosis virus. Gaps The DNA sequence is that of a cloned gene derived from a granulosis toxicant compsns. (also contg. biological and/or synthetic chemical insecticides) by rapidly degrading the peritrophic membrane lining 2824 cgattgtgttttcgtattcgcgccgtggcaacgagccgatgacacccgaaca 2875 2824 cgattgtgttttcgtattcgccgtggcaacgagccgatgacacccgaaca 2875 The VEF gene and protein can be used to ö 20; Mismatches 51; Indels 0; 281 ARCCNGTNGTNCCNAAYGCNCCNCCNGCNTAYGARAARYTNWSNGCNGARCA 332 Cloned gene isolated from a granulosis virus - enhances virus efficacy of viral pesticides, insecticides, biopesticides and virus and encodes a polypeptide viral enhancing factor which enhances infectivity of baculoviruses. The VEF improves the Score 132; DB 11; Length 3556; Pred. No. 6.04e+00; 935 T; Score 132; DB 4; Length 3556; Pred. No. 6.04e+00; 20; Mismatches 51; Indels 837 G; 840 G; infection of host insects, useful in pesticides protect plants or as components of pesticides. Sequence 3556 BP; 969 A; 815 C; 835 812 C; (BOYC-) BOYCE THOMPSON INST PLANT RES. Location/Qualifiers 'note= "baculovirus late promoter" Claim 2; Fig 3; 18pp; English. 969 A; Q28100 standard; DNA; 3556 BP the mid-gut lumen of insects. 9.3%; Best Local Similarity 36.6%; Best Local Similarity 36.6%; 11-FEB-1993 (first entry) 41; Conservative 41; Conservative Granados RR, Hashimoto Y; WPI; 92-301613/37. 434..3140 427..432 06-MAY-1991; 107278. 04-MAR-1991; US-663560. lepidopterous larvae. P-PSDB; R26790 09-SEP-1992. EP-502236-A /\*tag= a /\*tag= b Query Match promoter Sequence Query Match Matches Matches ខ្លួ a g à Š 임 ð

kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 KD (calculated Mr-114, 952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English. 8.9%; Score 126; DB 2; Length 1047; 13.4%; Pred. No. 1.45e+01; 51 T; 83 G 'note= "binds natriuretic peptides A,B and C]' hyperaldosteronism; glaucoma; guanyl cyclase. /note= "GC and protien kinase activity" 15 C; 09-APR-1991 (first entry) Human Natriuretic Peptide Receptor B. Location/Qualifiers 87 A; /label= transmembrane domain Domain 479..1047 /label= cytoplasmic domain /label= extracellular domain Chang M, Goeddel D, Lowe D; 456..456 Modified -site 161..163 Modified -site 244..246 Modified -site 277..279 /label= N-glycos site Modified -site 600..602 Modified -site 195..197 Modified -site 349.351 /label= signal sequence 23..455 23-JUN-1989; US-370673. Modified -site 24..26 /label= N-glycos site Modified -site 35..37 (GETH ) GENENTECH INC. /label= N-glycos site /label= N-glycos site /label= N-qlycos site /label= N-glycos\_site /label= N-glycos\_site /label= N-glycos\_site 22-JUN-1990; U03586. 1047 BP; label= mature NPBR WPI; 91-036711/05. N-PSDB; Q10324. Homo sapiens. also be prepd 10-JAN-1991. WO9100292-A. Sequence Query Match Protein Peptide Domain Oomain A STATE STAT

; ;

Gaps

2;

90; Mismatches 167; Indels

Best Local Similarity 13.4%; 40; Conservative

Matches

2

RESULT

δ

103 GTNATHYTNGGNGTNYTNYTNYTNATHGGNTGYTGGTAYTGYMGNMGNAGGNTAY 162

529 tahgkynnnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngaend

g

ð

43 AARGGNCAYGGNCAYWSNTAYACNACNGCNGARGARGCNGCNGGNATHGGNATHYTNACN 102

g

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<del>:</del>:

707 vysngnnnnnanrsgnnynngndnsnknnvnkvrngnrnynrnsndrtnnnnnnmm 765 :: | | :: | | :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

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07-FEB-1994 (first entry)
Sequence of tomato polyphenol oxidase (PPO) cDNA pPPO-T1.
Plant polyphenol oxidase; copper metalloenyme; phenol oxidation; ss.

Q46064 standard; cDNA; 1761 BP

Location/Qualifiers 1..1761

Lycopersicon esculentum.

589 nnnncnvtnycnrgsnndnnnndsnnndwmnry-snnndnvkgmannhnsnnsshgsnks 647

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US-08-231-565A-2 mg

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Aug 27 18:30

BP.

LT 12 Q05766 standard; DNA; 3561

RESULT ID Q0

7	COLOR Scalldalu, DINA, 3301 BF.
A F	QUS/66; 04_TAN=1991 (first entrv)
E	Sequence encoding viral enhancing factor (VEF).
KW	al insecticide; ds;
So	Tricoplusia ni granulosis virus (Tn GV).
ı E	Ney Location/gualiters CDS 4333132
FT	/*tag= a
Z.	EP-384294-A.
2. E	-AUG-1990.
7 8	13-kE6-1990; 102939. 21-EE6-1980: 116-31328
PA	PSON B INST
ΡΙ	Granados RR, Hashimoto Y;
H I	WPI; 90-262346/35.
<b>8</b> 8	
7 L	Gene Irom irrenoplusia in granutosis virus - enhances biological activity of virus infection in host insects.
Sa	Disclosure; Fig 3; 14pp; English.
ນ	Protein product may be be used as an additive to viral inseticides.
ဗ္ဗ	ansform plants
ဗ	_
38	to produce the VEF. Sequence 3561 BP; 969 A; 1037 C; 617 G; 938 T;
ð	8.9%; Score
æ ×	Best Local Similarity 35.4%; Pred. No. 1.26e+01; Matches 40; Conservative 21; Mismatches 52; Indels 0; Gaps 0
Dp	2759 gtccccactcgtacttcgatactttgtattttaaagtggagttgcgccaccaaaaccgtc 2818
•	
ð	221 GYCCNCARGARGGNTTYGAYCAYMGNGAYWSNAARGTNWSNYTNCARGARAARAAYTGYG 280
Op	2819 cgattgtgtttttgtattcgccgcgtggcaacgagccgatgacacccgaacag 2871
ò	281 ARCCNGINGINCONANGONCONCONGONTANGARAARYINWSNGCNGARCAR 333
į	
RESULT	13
2 2	046806 standard; DNA; 29879 BP.
E E	22-DEC-1993 (first entry)
E	chromosome.
Ž	eryA; biosynthesis; pol
2 2	erytnromycin; condensation; elongation; acyl chain growth; gene replacement: ss.
0.5	carapolyspora
표단	Key Location/Qualifiers
E	aq≕ a
FT	ORF 1"
FI	CDS 1021820921
E	/ ray= n /note= "ORF 2"
E	
I	/*tag= c /note= "ORF 3"
PN	W09313663-A.
PD	22-JUL-1993. 17-Jan-1902. HODA27
P.B.	17-JAN-1992; WO-U00427.
PA	(ABBO ) ABBOTT LAB.

ö

15; Mismatches 26; Indels 0; Gaps

Best Local Similarity 40.6%; Matches 28; Conservative

Query Match

Score 127; DB 8; Length 1761; Pred. No. 1.26e+01;

511 T;

375 G;

496 A; 379 C;

downstream portion is Q46066. Sequence 1761 BP; 496 A;

97 aaaccctct 105

37 ttatgcaccaacaaatccctctcttcttccttcaccaccaactcatccttgttatca 96

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Example, pages 27-28, 49pp; English.

To obtain PPO mRNA for construction and screening of a cDNA expression library, mRNA was obtd. from leaflets and petioles of identic of pPPO-TI is expressed in trichome and epidemal cells, and pPPO-TI is expressed in trichome and epidemal cells, and pPPO-TI is given in Q46064/R39553. The upstream portion immediately prior to the ATG start codon is Q4605, and the

Cloning and sequencing of plant polyphenol oxidase cDNA - useful for genetic transformation of plants to achieve e.g. herbivore

resistance

(CORR ) CORNELL RES FOUND INC.

Steffens JC; WPI; 93-272433/34. P-PSDB; R39553.

31-JAN-1992; US-833839

29-JAN-1993; U00869.

/\*tag= a WO9315599-A. 19-AUG-1993.

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0; 19337 cgacgagtccgcggatctgctcgccgaggacggcgtcttcgtcgagatgggcaagaccga 19396 those inactivating a single function in a module which does not arrest acyl chain growth; those inactivating a single function in a module which does affect chain growth; and those affecting an entire module. The mutations may be introduced by gene replacement. Sequence 29879 BP; 3672 A; 10596 C; 11545 G; 4066 T; of one condensation step. The precise succession of elongation steps is dictated by the genetic order of the modules. This fragment may be specifically altered such that novel polyketide molecules of desired structure are produced. Three types of alteration may be produced; erythromycin. eryA is organised in modules and each module takes care This sequence represents a fragment of the Saccarapolyspora erythraea 289 CNACNGGYTCRCARTTYTTYTCYTGNARNWSNACYTNWSRTCNCKRTGRTCRAANCCYT 230 17; Mismatches 25; Indels 0; Gaps Flavin adenine mononucleotide; nitroreductase; mutagen; carcinogen; genome, designated  $\ensuremath{\operatorname{ery}} A$  . The polypeptides encoded by this region are involved in the biosynthesis of the polyketide segment of cpds. - by introducing altered biosynthetic gene-contg. DNA into Enzyme with flavin reducing and nitro-reductase activity - obtained from Vibrio fischeri, useful in fluorescent diagnostic Biosynthesis of specific polyketide analogues esp. erythromycin Query Match 8.9%; Score 127; DB 7; Length 29879; Best Local Similarity 38.2%; Pred. No. 1.26e+01; /\*tag= a /note= "generated from the amino acid sequence R38098 of V.fischeri ATCC 7744 FMN luminescent bacteria; Vibrio fischeri; ss. Degenerate FMN reductase coding sequence. reductase; the (claimed) coding sequence printed in the specification contained non-IUPAC degenerate codons which were converted to IUPAC equivalent for this Location/Qualifiers McAlpine JB; Claim 27; Fig 2; 133pp; English. Inouye S, Kanoh H, Zenno S; Q43519 standard; DNA; 657 BP 22-0CT-1993 (first entry) 26; Conservative 16-DEC-1992; 311476. 16-DEC-1991; JP-351717. 16-OCT-1992; JP-279029. 1..656Katz L, 19397 cctgcggg 19404 (CHCC ) CHISSO CORP WPI; 93-198848/25. P-PSDB; R44430-32. Donadio S, Katz I WPI; 93-242804/30. 229 CYTGNGGR 222 microorganisms P-PSDB; R38098. EP-547876-A. 23-JUN-1993. Synthetic. Query Match 043519; record" assays Matches g ď g g ID DAC ON SET THE FET THE FET

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ö ö been converted to the IUPAC codons for inclusion in GENESEQ. Bacteria containing the FMN reductase gene will be useful indicators for 501 hgayccngarytnytnwsngarathttygcngaygarytnaarggntaygartgycaygt 560 561 ngcnytngcnathggntaycaycayccnwsngargaytayaaygcnwsnytnccnaarws 620 242 TGRTCRAANCCYTCYTGNGGRCANCKNGKNGTNARNGCRCAYTGNGTNCCNACRTGNARN 183 182 WSYTTRICCATNARNGCNCKRTANCCRTTNCKNCKRCARTACCARCANCCDATNARN 123 Gaps 0; Gaps (043520). A degenerate coding sequence was generated from the amino Claim 1; Fig 1; 20pp; English.
A 218 amino acid protein (see R38098) of mol.wt. 24562 and having nitroreductase and flavin reducing activity typical of luminescent bacteria was deduced from a V.fischeri ATCC 7744 coding sequence mutagens and carcinogens (e.g. nitroarenes) in fluorescent assays. acid sequence and claimed. The sequence as printed in the specification contained non-standard degenerate codons which have Sardine; osteoporosis; osteoblasis; pro-osteoblasis; activation; differentiation; treatment; degenerate; ss. peptide. The peptide has a (pro-) osteoblast differentiation and activation effect, and a pref. dosage of 0.1-5 mg/kg/day. Sequence 159 Bp; 28 A; 19 C; 31 G; 15 T; differentiation and activation effect, isolated from sardine or .**;** 24-JAN-1996 (first entry) Degenerate sardine derived osteoporosis treatment peptide DNA. Q94404 encodes R77778 a sardine derived osteoporosis treatment 8.6%; Score 122; DB 16; Length 159; 2.9%; Pred. No. 2.58e+01; Query Match 8.7%; Score 123; DB 7; Length 657; Best Local Similarity 9.4%; Pred. No. 2.24e+01; Matches 12; Conservative 45; Mismatches 70; Indels Peptide for osteoporosis treatment - has (pro-) osteoblast 35; Mismatches 53; Indels 80 T; 94 G; 67 C; Location/Qualifiers :: :: -: (SUMQ.) SUMITOMO METAL IND LTD. WPI; 95-203835/27. P-PSDB; R77778. Claim 1; Page 6; 9pp; Japanese. 138 A; Q94404 standard; DNA; 159 BP. Best Local Similarity 12.9%; 13; Conservative Sardinops melanostictus. 1..159 22-0CT-1993; JP-265163. 22-OCT-1993; 265163 See also Q49058-9. 122 ARNARNA 116 621 nmgnaar 627 J07118296-A. mat peptide 09-MAY-1995. /\*tag= a Sequence Query Match goldfish Query Match 094404; Matches 쇰 g g S

54 rgcnmgnmgnytnytngaygcnathgtnaargarttygtncaratgacngcngargayyt 113 : : : : : | | | | | | ::: 133 GGNWGSRTANGCGNGGNWGSTTGYTCYTCNGCNWSNARYTTYTCRTANGCNGGNGGNGCRTTN 294

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Search completed: Tue Aug 27 18:42:40 1996 Job time : 44 secs.

US-08-231-565A-2 rat

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols MPsrch\_tpn

Tue Aug 27 18:43:02 1996; MasPar time 164.99 Seconds 762.445 Million cell updates/sec

Tabular output not generated.

Run on:

>US-08-231-565A-2 Description:

Title:

N.A. Sequence:

Comp:

1 ATGCCHMGNGARGAYGCNCA......SNCCNCCNCCNTAYMSNCCN 354 TACGGNKCNCTYCTRCGNGT.......mnGGNGGNGGNATRSFNGGN (1-118) from US08231565A.pep 1420 Perfect Score:

Scoring table:

TABLE bktranslate2 Gap 30

509049 seqs, 177673129 bases x 2 Searched:

Dbase 0; Query 0

STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

15:EST12 10:EST16 11:EST17 18:EST18 19:EST19 20:EST20 21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 23:EST23 24:EST27 28:EST28 24:EST29 24:EST24 25:EST25 26:EST26 23:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38 39:EST39 40:EST46 41:EST41 42:EST42 43:EST43 44:EST44 45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50 51:EST51 52:EST55 56:EST56 57:EST57 58:EST58 59:EST56 66:EST66 67:EST6 67:EST76 67:EST76 67:EST76 77:EST77 77:EST77 78:EST78 74:EST74 74:E 1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 EST-STS

Database:

118:gnEST10 119:gnEST11 120:gnEST12 121:gnEST13 122:gnEST14 123:gnEST15 124:gnSTS1 125:gnSTS2 126:enEST1 98:EST91 99:EST92 100:EST93 101:EST94 102:EST95 103:EST96 104:EST97 105:EST98 106:EST99 107:EST100 108:EST101 109:qnEST1 110:qnEST2 111:qnEST3 112:qnEST4 113:qnEST5 114:qnEST6 115:qnEST7 116:qnEST8 117:qnEST9

Aug 27 18:33

127:enEST2 128:enEST3 129:enEST4 130:enEST5 131:enEST6 132:enEST7 133:enEST8 134:enEST9 135:enEST10 136:enEST11

Mean 61.375; Variance 71.660; scale 0.856 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		10				
Result No.	Score	Query Match	Query Match Length DB	GI	Description	Pred. No.
-	1392	0.86	=	3 N23770	vx35a12.rl Homo sapie	0.00e+00
. ~	1392		593 13	6 HS770	al2,rl Homo sapi	8
· m	1271	6	Ξ	7 N35680	05.rl Homo s	
4	1271		-	HS 6802	rl Homo s	
. Z	1205	4	393 135	HS 6562	rl Homo	
•	1205		П	N36656	.rl Homo a	0
7	947			H	Home sapi	4.34e-264
ထ	722				2.81 Homo	1.83e - 186
	722				.sl Homo	Ψ.
c 10	640		433 135		s Homo s	1.17e-158
	640	_			sl Homo	_
		_			sl Homo s	
		38.0			sl Homo	•
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				N26562	sl Homo	5.89e-122
16		10.8			sl Homo	.17e-0
17			312 109		yv15c06.s1 Homo s	2.17e-09
18		•		-	dopsis	2.17e-09
19	136	9.6	43 117	N36215	Homo	.14e-0
20					1 Home	1.14e - 05
c 21		9.3	411 45		Ношо	7.70e-05
		9.5		H27083	Ношо	1.97e-04
c 23				H26878	Ношо	٠,
				N429	1 Homo	1.97e - 04
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3.2	126			R59572	097h10.sl Homo san	.24e-0
	125				Нопо	9
m	123			HUM13	l brai	4.77e-03
c 35	122			R95571	SMNHADA008030SK Schis	$\overline{}$
	122			_	a napus	
٣	122			HSC2PH091	H. sapiens partial cD	7.43e - 03
c 38	122	8.6	300 77	T00011	EST00732 Caenorhak	7.43e - 03
m	122			HHEF052		7.43e - 03
4	122		320 73		019T3 Schi	7.43e-03
4	122			H62105	Homo &	0-a
-	122			T960	1 Home	7.43e-
4	122		23	H61302	.rl Homo s	6-0
c 44	122	9.8	442 10	T955	s.sl Homo	7.43e
4	122	9.6	28	T5532	yb47h10.sl Homo sapie	7.43e - 03

ALI GNMENTS

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LOCUS N2	N23770 593 bp mrna est · 28-dec-1995	d d	175 ctgctcatcggctg
DEFINITION yx ACCESSION N2	yx35a12.rl Homo sapiens cDNA clone 263710 5′. N23770 A113020	β	:  :  :           121 YTNYTNATHGGNTG
ORDS	91.0.720 EST balana_020710i=i=a_a7 libana_i=fanana anlananata Onthun	ΩP	235 agtcttcatgttgg
SOURCE NO	numan clone-rollo pimeral, inbrary-source metanocyce known vector=pTT3D (Pharmacia) with a modified polyinker het=DHIOB	δy	181 WSNYTNCAYGINGG
<u>ස</u> පි	(ampicillin resistant) Kaitel=Not I Kaite/=Eco KI Male. 18t strand cDNA was primed with a Not I - oligo(dT) primer	qo	295 categggacagcaa
<u>5</u> ] op	[5'-TGTTACCAATCTGAAGTGGGACGGCCGCAGTTTTTTTTTT	Qy	::    ::    241 CAYMGNGAYWSNAA
(P RI	(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library	qa	355 ccacctgcttatga
8.5	constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanovyes (FS374) was kindly provided by Dr. Anthony P.	ò	301 CCNCCNGCNTAYGA
AL	Albino	7	
	nomo Baprens Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;	RESULT	LT 2
De De	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;	OI	HS770262 standard
Sa	Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Enthosis: Archants: Drimatos: Catarhis: Usminidas: Usm	AC	N23770; 29_DEC_1005 /Bel A
	(bases 1 to 593)	DT	29-DEC-1995 (Rel. 4
AUTHORS Hi	illier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,	36 S	yx35a12.rl Homo sap
E C	otman,m., Hutcman,m., Nucaba,T., Le,m., Lennon,e., Marra,m., arsons.J., Rifkin,T., Rohlfind.T., Soares.M., Tan.F.,	SO	Homo sapiens (human
I	Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and	30	Eukaryota, Animalia
	Wilson, R.	00	Theria; Eutheria; P
JOURNAL UN	ine wasnu-merck toi rroject Unpublished (1995)	RP RP	1-593
		RA	Hillier L., Clark N
ပ အာ	Contact: Wilson RK Washil-Merck FST Project	R &	Holman M., Hultman Parsons J., Rifkin
e Ba	Washington University School of Medicine	RA	Trevaskis E., Water
<b>4</b>	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	RT	"The WashU-Merck ES
re Fa	ren: 314 286 1810	2 8	Contact: Wilson RK
mg.	Email: est@watson.wustl.edu	S	School of Medicine
H	High quality sequence stops: 414	88	MO 63108 Tel: 314 2
Z. Th	cource: IMAGE CORSOICIUM, DAND This clone is available royalty-free through LLNL ; contact the	38	Consortium, LLNL Th
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FEATURES	NUBL 91: 113/92U Location/Qualifiers	FF FF	vey roc
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BASE COUNT ORIGIN	165 a 140 c 137 g 146 t 5 others	ŎS	Sequence 593 BP; 16
Query Match Best Local Similarity	98.0%; Score 1392; DB 113; Length 593; Similarity 58.6%; Pred. No. 0.00e+00:	n e	Query match Best Local Similarity Matches 207; Conser
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RA 88	Hillie	Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Lolman M. Hultman M. Kuraha T. Ta M. Lannon G. Marra M.
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q	55 a	atgccaagagaagatgctcactcatctatggttaccccaagaaggggcacggccactct 114
Qy	1 4	ATGCCNMGNGARGAYGCNCAYTYATHTAYGGNTAYCCNAARAARGGNCAYGGNCAYWSN 60
q	115 t	tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 174
δy	61 1	TAYACNACNGARGARGARGCNCCNGGNATHGGNATHYTNACNGTNATHYTNGGNGTNYTN 120
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N35680 370 bp mRNA EST 16-JAN-1996 yx62h05.rl Homo sapiens cDNA clone 266361 5' similar to PIR:A55253 A55253 melanoma antigen MART-1 - human ; (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. (ampicillin resistant) Rsitel-Not I Rsite2-Eco RI Male. 1st strand double-stranded cDNA was size selected, ligated to Eco RI adapters Deuterostomia, Chordata, Vertebrata; Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. WSNYTNCAYGTNGGNACNCARTGYGCNYTNACNMGNMGNTGYCCNCARGARGGNTTYGAY 240 catcgggacagcaaagtgtctcttcaagagaaaaactgtgaacctgtggttcccaatgct 354 235 agtetteatgttggeaeteaatgtgeettaaeaagaagatgeeeacaagaagggtttgat 294 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., human clone=266361 primer=T7 library=Soares melanocyte 2NbHM Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 370) ccacctgcttatgagaaactctctgcagaacagtcaccaccaccttattcacc 407 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; cDNA was primed with a Not I - oligo(dT) primer Washington University School of Medicine /organism≂"Homo sapiens" High quality sequence stops: 337 Source: IMAGE Consortium, LLNL Location/Qualifiers Email: est@watson.wustl.edu The WashU-Merck EST Project WashU-Merck EST Project Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 NCBI gi: 1156822 1..370 Homo sapiens Wilson, R. q1156822 Albino. DEFINITION ORGANISM 181 295 241 355 AUTHORS 301 JOURNAL ACCESSION REFERENCE KEYWORDS FEATURES COMMENT SOURCE g g δ g ð Š .,

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/clone="266361" /note="human"

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5; 96 tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 155 156 ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaa 215 216 agtcttcatgttggcactcaatgtgc-ttaacaagaagatgcccacaagaagggtttgat 274 275 catcgggacagcaaagtgtctcttcaagagaaaaactgtgaacctgtggttcccaatgct 334 95 9 Gaps 36 atgccaagagaagatgctcacttcatcgttaccccaagaaggggcacggccactct 1 ATGCCNMGNGARGAYGCNCAYTTYATHTAYGGNTAYCCNAARAARGGNCAYGGNCAYWSN 5; Length 370; Indels Score 1271; DB 117; Pred. No. 0.00e+00; 78; Mismatches 59; 335 ccacctgcttatggagaaactctctgcagaacagtc 370 86 t T 4 HS680270 standard; RNA; EST; 370 ó 94 89.5%; 58.6%; 87 c 197; Conservative <1..>370 Best Local Similarity 103 Query Match BASE COUNT Matches 61 301 ORIGIN g g 음 g g δ ð 쇰 Š Š ð à

19-JAN-1996 (Rel. 46, Created) 19-JAN-1996 (Rel. 46, Last updated, Version 1) yx62h05.rl Homo sapiens cDNA clone 266361 5' similar to PIR:A55253 Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; A55253 melanoma antigen MART-1 - human ;. Homo sapiens (human) N35680; 

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est@watson.wustl.edu High quality sequence stops: 337 Source: IMAGE Consortium, LINL This clone is available royalty-free through LLNL Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: contact the IMAGE Consortium (info@image.llnl.gov) for further "The WashU-Merck EST Project"; .nformation. NCBI gi: 1156822 Unpublished

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122 tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 181 TAYACNACNGCNGARGARGCNGCNGGNATHGGNATHYTNACNGTNATHYTNGGNGTNYTN 120 182 cngctcatcggctgttggtatngtagaagacgaaatggatacagagccttgatggataaa 241 : :| ||:|| ||:|||||: ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||: 242 agtetteatgttggeaeteaatgtgeettaaeaagaagatgeeeaeaagaaggtttgat 301 302 catcgggacagcaaagtgtctcttcaagagaaaaactgtgnacctgtggggcccaatggg 361 241 CAYMGNGAYWSNAARGTNWSNYTNCARGARAARAAYTGYGARCCNGTNGTNCCNAAYGCN 300 63 atgccaagagaagatgctcacttcatctatggtnnccccangaagggcacgg-cactct 121 9 Gaps 2; Length 393; Indels Sequence 393 BP; 105 A; 94 C; 105 G; 81 T; 8 other; 67; DB 135; Score 1205; DB 13: Pred. No. 0.00e+00; 75; Mismatches || || || || ||:||:||:|| : : || ||:| CCNCCNGCNTAYGARAARYTNW-SNGCNGARC 331 362 ccacctgcttatgagaaactcttctgcagaac 393 ′organism="Homo sapiens" /clone="269080" /note="human" 84.9%; 56.6%; 188; Conservative <1..>393 Best Local Similarity Query Match 19 Matches 301 q g g ð FFFFS 2 ð 쇰 셤 à ð δ ð

yx91a09.rl Homo sapiens cDNA clone 269080 5' similar to PIR:A55253 A55253 melanoma antigen MART-1 - human ;. vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. 1st strand (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes; Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., human clone=269080 primer=T7 library=Soares melanocyte 2NbHM Irevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Homo sapiens q1157798 Wilson, R. Albino. 9 DEFINITION ORGANISM REFERENCE AUTHORS ACCESSION NID KEYWORDS RESULT SOURCE TOCUS

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TITLE JOURNAL COMMENT	The WashU-Merck EST Project Onpublished (1995)	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
· ·	Contact: Wilson RK WashU-Merck EST Project WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 7e1: 314 286 1810 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 169 Source: IRAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	REFERENCE 1 (bases 1 to 303) AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, MW., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, LI., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shilley, R., Spriggs, T.A., Utterback, T.R.,
FEATURES source	NCBI qi: 1157798 Location/Qualifiers 1.393   /organism="Homo sapiens" /clos="269080" /clos="269080"	Melaman, J. T., Dedulally, J. Cachi, Captur, Captur, Captur, C., Clains, F. Callins, E. Cachen, T.A., Collins, E. Callins, E. Cachen, Fischer, C., Hastings, G.A., He, WM., Hu, JS., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meisener, P.S., Olsen, H., Raymond, L., Wel, YF., Wing, J., Xu, C., Yu, GL., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
mRNA BASE COUNT ORIGIN	105 a	TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence JOURNAL Unpublished (1995)
Query Match Best Local Matches 1	Query Match 84.9%; Score 1205; DB 117; Length 393; Best Local Similarity 56.6%; Pred. No. 0.00e+00; Matches 188; Conservative 75; Mismatches 67; Indels 2; Gaps 2;	
0b 63 a	3 atgccaagagaagatgctcacttcatctatggtnnccccangaaggggcacgg-cactct 121        :    :  :  :  :  :  :   :      :  :	Fax: 3018699423 Email: tdbinGtdb.tigr.org For clone auxilability, additional sequence and expression information related to this EST plasse contact the TITR Database
Db 122 t     Qy 61 1	122 tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtctta 181   :              :  :              :	(tdbinfoldtd). Italian (tdbinfoldtd).  NCBI gi: 609987
0b 182 c	182 cngctcatcggctgttggtatngtagaagacgaaatggatacagagccttgatggataaa 241 : :    :     :     :  :  :  :     :     :     :     :    :   :  :	rce B
Db 242 a	242 agtetteatgttggeacteaatgtgeettaacaagaagatgeecacaagaaggtttgat 301 :: :    :           :  :   :          :  :	r 81 a
302	catoggacagcaaagtgtctcttcaagagaaaaactgtgnacctgtggggcccaatggg 361	Query Match 66.7%; Score 947; DB 82; Length 303; Best Local Similarity 59.7%; Pred. No. 4.34e-264; Matches 145; Conservative 53; Mismatches 45; Indels 0; Gaps 0;
362	362 ccactgcttatgagaaactcttctgcagaac 393 	Db 56 atgccaagagaagatgctcactcatctgttgctcacgcaagaaggggaacggccactc 115
SULT		Db 116 tacaccacggctgaagaggccgctgggatcggcatcctgacagtgatcctgggagtntta 175   1:1
DEFINITION ACCESSION	12,1084 50.5 pp many EST19370 Homo sapiens cDNA 5' end similar to Human recognized by T-cells (MART-1) mRNA. (HT:4028). T27884	Db 176 ctgctcatcggctgttggtattgtagaagacgaaatggatacagagccttgatggataaa 235 :  :       :     :     :   :  :       :     :
KEYWORDS SOURCE ORGANISM		Db 236 agtcttcatgttggcactcaatgtgccttaacaagaagatgcccacaagaaggtttatt 295 :::   :

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

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yx36a12.s1 Homo sapiens cDNA clone 263806 3', N20091

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177

4;

Gaps

Indels 4; Length 473;

1 others

human clone=263806 primer=m13 -40 forward library=Soares melanocyte double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. ggtggataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattg 296 297 ggaaccacaggttcacagtttttctcttgaagagacactttgctgtcccgatgatcaaac 356 1 (bases 1 to 473)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Irevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker RI sites of a modified pT7T3 vector (Pharmacia). Library 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 49; Mismatches 53; Washington University School of Medicine Score 722; DB 112; Pred. No. 1.83e-186; = 151 /organism≃"Homo sapiens" Email: est@watson.wustl.edu High quality sequence stops: 363 Location/Qualifiers ρ The WashU-Merck EST Project 97 /clone="263806" WashU-Merck EST Project /note="human' 50.8%; 55.3%; 97 c 131; Conservative Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 <1..>473 NCBI gi: 1124758 1.473Homo sapiens Best Local Similarity Wilson, R. 127 Albino. Query Match source ORGANISM BASE COUNT TITLE JOURNAL Matches 237 KEYWORDS SOURCE REFERENCE AUTHORS FEATURES ORIGIN 유 g 셤 g ggaaccacaggttcacagttttctcttgaagagacactttgctgtcccgatgatcaaac 356 237 ggtggataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattg 296 ccttcttgtgggcatcttcttgttaagggcacattngagtgccaaccatggaagactttt 416 Gaps Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., estewatson.wustl.edu High quality sequence stops: 363 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further 417 atccatcaaggctctgtatccatttcgtcttctacaataccaacagccggtgagcag 473 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: 4; Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Length 473; 49; Mismatches 53; Indels Sequence 473 BP; 127 A; 97 C; 97 G; 151 T; 1. other; Score 722; DB 129; Pred. No. 1.83e-186; 17-DEC-1995 (Rel. 46, Created) 17-DEC-1995 (Rel. 46, Last updated, Version 1) yx36a12.s1 Homo sapiens cDNA clone 263806 3' /organism="Homo sapiens" T 8 HS091255 standard; RNA; EST; 473 BP. Location/Qualifiers /clone="263806" /note="human" "The WashU-Merck EST Project"; information. NCBI gi: 1124758 50.8%; 131; Conservative

Lócal Similarity

Matches

셤 გ g S 음 g g g,

297

357

Query Match

mRNA

Aug 27 18:33

US-08-231-565A-2 rat

2

ACCESSION N24677  NID 91138827  KEYWORDS EST.  SOURCE human clone=269080 primer=m13 -40 forward library=Soares melanocyte  ZOURCE humb vector=p17730 (Pharmacia) with a modified polylinker in the property in the property of the performance of	host-BHIOB (amplicitin resistant) RSITES-ENG KI Male.  1st strand cDNA was primed with a Not I - oligo(dT) primer  [5'-TGTMACCAATGTGGAGGGGGGGGGGGGGTTTTTTTTTTTT	CE RS	COMMENT Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 Email: est@Matson.wustl.edu High quality sequence stops: 315 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@limage.llnl.gov) for further information.	CBI gi: 1138827 Location/Qualifiers 1.433 /organism="Homo sapiens" /clone="269080" /note="human" <1>433 119 a 85 c 86 g 142 t	Query Match 45.1%; Score 640; DB 113; Length 433; Best Local Similarity 56.8%; Pred. No. 1.17e-158; Matches 108; Conservative 36; Mismatches 45; Indels 1; Gaps 1; Db 244 ataaggtggtggtggtgttctggagaggttctctataagcaggtggagcattgggaac 303 :
Db 417 atccatcaaggctctgtatccatttcgtcttctacaataccaacagccggtgagcag 473 	RESULT 10  ID HS677260 standard; RNA; EST; 433 BP.  AC N24677; DT 30-DEC-1995 (Rel. 46, Created) DT 30-DEC-1995 (Rel. 46, Last updated, Version 1) DE yxgla09.sl Homo sapiens CDNA clone 269080 3'.  KW EST.  OS Homo sapiens (human) OC Eukaryots; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; OC Thoris: Estheryots; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;		CC est@watson.wustl.edu High quality sequence stops: 315 Source: IMAGE CC consortium, LIAL This clone is available royalty-free through LINL CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further CC information. NCBI gi: 1138877 EH Key Location/Qualifiers FT Lource 1433 FT /organism="Homo sapiens" FT /note="human"	Query Match         45.1%; Score 640; DB 135; Length 433;           Best Local Similarity 56.8%; Pred. No. 1.17e-158;           Matches 108; Conservative 36; Mismatches 45; Indels 1; Gaps 1;           Db 244 ataaggtggtggtgactgttctgcagaggtttctcataagcaggtggagcattgggaac 303           :	Cp 288 NACNGGYTCRCARTTYTTYTCYTGNARNWSNACYTIWFSRTCRCKTAANCCYT 230  Db 364 cttgtgggcatcttcttgttaaggcacattgagtgccaacatgaagacttttatccatca 423   :

229 CYTGNGGRCANCKNCKNGTNARNGCRCAYTGNGTNCCNACRIGNARNWSYTTRICCATNA 170

US-08-231-565A-2.mi

human clone=269707 primer=m13 -40 forward library=Soares melanocyte (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Eukaryofae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 396)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Iennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. ö This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. 244 ataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattgggaac 303 348 RTANGGNGGNGGNASYTCYTCRTANGCNGGNGCRTTNGGNAC 289 304 cacaggttcacagtttttctcttgaagagacactttgctgtcccgatgatcaaacccttc 363 Gaps Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 .**,** Length 396; 2 others Indels 29; Mismatches 36; Score 540; DB 113; Pred. No. 2.94e-125; 131 t 364 ttgtgggcatcttcttgttaaggcacattgag 395 228 YTGNGGRCANCKNGTNARNGCRCAYTGNG 197 /organism="Homo sapiens" Email: est@watson.wustl.edu High quality sequence stops: 310 Source: IMAGE Consortium, LLNL Location/Qualifiers б The WashU-Merck EST Project 80 /clone="269707" /note="human" WashU-Merck EST Project 38.0%; 57.2%; 75 c Contact: Wilson RK 87; Conservative Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 <1..>396 NCBI gi: 1138946 1..396 Query Match Best Local Similarity Homo sapiens Wilson, R. 108 source ORGANISM TITLE JOURNAL BASE COUNT Matches REFERENCE FEATURES COMMENT ORIGIN SOURCE 쇰 g 음 გ 쇰 ც

> Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hohman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., "The WashU-Merck EST Project";

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae

Homo sapiens (human)

30-DEC\_1995 (Rel. 46, Created) 30-DEC-1995 (Rel. 46, Last updated, Version 1) yx97f10.s1 Homo sapiens cDNA clone 269707 3'.

standard; RNA; EST; 396 BP.

HS796259

N24796;

169 RNGCNCKRTA 160

424 aggetetgta

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estëwatson.wustl.edu High quality sequence stops: 310 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further

Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

Unpublished

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Gaps

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29; Mismatches 36; Indels

Length 396;

Score 540; DB 136; Pred. No. 2.94e-125;

38.0%;

Best Local Similarity

Query Match

87; Conservative

Matches

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BP; 108 A; 75 C; 80 G; 131 T; 2 other;

Sequence 396

IIRNA

/organism="Homo sapiens"

source

/clone≂"269707" /note="human"

Location/Qualifiers

information. NCBI gi: 1138946

244 ataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattgggaac 303

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348 RTANGGNGGNGGNWSYTGYTCNGCNWSNARYTTYTCRTANGCNGGNGGNGCRTTNGGNAC 289

288 NACNGGYTCRCARTTYTTYTCYTGNARNWSNACYTTNWSRTCNCKRTGRTCRAANCCYTC 229

 28-DEC-1995

yx97f10.s1 Homo sapiens cDNA clone 269707 3'

ñ24796 g1138946

396 bp

N24796

RESULT

DEFINITION

ACCESSION NID KEYWORDS

14

RESULT

US-08-231-565A-2 rst

US-08-231-565A-2 rat

244 ataaggtggtggtgactgttctgcagaggtttctcataagcaggtggagcattgggaac 303 348 RTANGGNGGNGGNWSYTGYTCNGCNWSNARYTTYTCRTANGCNGGNGGNGCRTTNGGNAC 289 364 ttgtgggcatcttcctgttaaggcacattgag 395 228 YTGNGGRCANCKNGTNARNGCRCAYTGNG 197 Search completed: Tue Aug 27 18:46:01 1996 Job time: 179 secs. Query Match 37.3%; Best Local Similarity 57.2%; 87; Conservative source ORGANISM BASE COUNT TITLE JOURNAL Matches REFERENCE AUTHORS FEATURES COMMENT ORIGIN g გ 움 გ 음 გ ö 244 ataaggtggtggtgactgttctgcagagagtttctcataagcaggtggagcattgggaac 303 304 cacaggttcacagtttttctcttgaagagácactttgctgtcccgatgatcaaacccttc 363 348 RTANGGNGGNGGNWSYTGYTCNGCNWSNARYTTYTCRTANGCNGGNGGNGCRTTNGGNAC 289 est@watson.wustl.edu High quality sequence stops: 305 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further Gaps 29-DEC-1995 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., "The WashU-Merck EST Project"; Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: ; 0 Homo sapiens (human) Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Score 530; DB 134; Length 401; Pred. No. 5.89e-122; Indels N26562 401 bp mRNA EST yx62h05.s1 Homo sapiens cDNA clone 266361 3' Sequence 401 BP; 110 A; 79 C; 82 G; 129 T; 1 other; 28; Mismatches 37; 30-DEC-1995 (Rel. 46, Created) 30-DEC-1995 (Rel. 46, Last updated, Version 1) yx62h05.s1 Homo sapiens cDNA clone 266361 3'. 364 ttgtgggcatcttcctgttaaggcacattgag 395 228 YTGNGGRCANCKNGTNARNGCRCAYTGNG 197 /organism="Homo sapiens" standard; RNA; EST; 401 BP Location/Qualifiers /clone="266361" information. NCBI gi: 1140910 /note="human" 37.3%; 57.2%; Local Similarity 57.2%; es 87; Conservative <1..>401 N26562 g1140910 Unpublished HS562267 Query Match N26562; source DEFINITION 1 - 401**IIRNA** Matches ACCESSION KEYWORDS SOURCE RESULT

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Gaps

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constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Hillier, L., Clark, N., Dubuque, T., Ellieton, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. RI sites of a modified pT7T3 vector (Pharmacia). Library 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Length 401; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; 1 others Score 530; DB 114; Length 4 Pred. No. 5.89e-122; 28; Mismatches 37; Indels Washington University School of Medicine 129 t /organism="Homo sapiens" High quality sequence stops: 305 Source: IMAGE Consortium, LINL Location/Qualifiers ð Email: est@watson.wustl.edu The WashU-Merck EST Project 83 /clone="266361" Contact: Wilson RK WashU-Merck EST Project /note="human' 79 c (bases 1 to 401) Unpublished (1995) Fax: 314 286 1810 Tel: 314 286 1800 <1..>401 NCBI gi: 1140910 1..401 Homo sapiens Wilson, R.

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn Tue Aug 27 08:43:36 1996; MasPar time 1419.91 Seconds 1162.639 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-231-565A-26 (1-2172) from US08231565A.seq 2172 Title:

Description:

Perfect Score:

CACCTGCCGGTAATGGTTAG.......TITTTTTTTTTTTTTTTT N.A. Sequence: COMD:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 270440 seqs, 380027776 bases x 2 Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

embl-new3 Database:

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PR11 10:PR12 11:PR0 12:ROD 13:SYN 14:UNC 15:VRT 16:VIR1 17:VIR2

genbank92 Database:

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCC8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5 32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG 39:PLM1 40:PLM2 41:PLM3 42:PLM4 43:PLM5 44:PLM6 45:PLM7 46:PLM8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI6 53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12 59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6 66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3 73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PLN 86:PRI 87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT u-emb145 92 qenbank-new1

Database:

Database:

93:part1

Mean 12.523; Variance 9.406; scale 1.331 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

US-08-231-565A-26.rgc Aug 27 08:56

SUMMARIES

Pred. No.	0.00e+00					•		0.00e+00	•	3.61e-110	5 8	1.98e-90	.46e-	.46e-5	8e-2	.58e-2	2,58e-26	. 58e-	•	5.98e-06	1.60e-05	1.60e-05	1,60e-05	•		•	<b>7</b> -	1.136-04		_	1.13e - 04	3e-	Э́е-	.13e-	.13e	1.13e - 04	∹	1.13e - 04	13e-	<u>۾</u>	송.	1.13e-04
Description	gp100=melanocyte line	те 20п	Pmel 17 mRNA	Human melanocyte-spec	ţ,	l pigme		melanocyte	melanocyte	Human melanocyte prot	me lanocyte	melanocyte	melanocyte			Human melanocyte prot		Human melanocyte-spec	R.norvegicus mRNA for	Rat D-binding protein	glycine-rich protein	.lacryma-jobi mRNA	_		isum sativum chlor	sapiens mKN	LOE	Chicken troponin C (T	CKII beta m	APC=tumor suppressor,	c-erbB3=receptor tyro	Mouse mRNA for MyD118	Mus musculus glutathi	Cricetulus griseus (c	18 mRNA		heat translation		.discoideum mRNA	.discoideum mRNA	z	Drosophila Knrl gene
OI	S73003	HSU01874	HUMPMEL	HSPMEL17S2	HSMEL17S2	BOVBRPEIA	MMU14133	HSMELU3	HSPMELUS	HSMELUS HSPMF105	HOPWET OA	HSMELO4	HSPMEL02	HSMEL02	HSMEL01	HSPMEL01	HSPMEL17S1	HSMEL17S1	RNRNASYNV	RATDBPA	S47413	CLJACOIV	BNPNL2	S59519	PEA 70HSP	HSBINDPR	HS 2 3 ABP	DDE428	SSCKIIB	578214	S61953	MMMYD118	MM4 0808	CCTUBB3		EMCOLNF13	WHTTEF1X	RRPCP3145	DDRNAPAT1	DDRNAPAT1	RNMOBP81P	DMKINR1
DB	59	22	23	98	2	33	19	2 2	9 5	2 %	9 0	2 2	98	12	10	98	98	10	99	<b>7</b> :	43	40	39	6/	47	200	2° c	87 [	34	59	29	13	12	9	78	30	45	99	81	Ŋ	12	53
Length	2130	2026	2131	2817	2817	1584	1881	2001	7007	11 /8	1550	1559	673	673	577	577	3109	3109	1620	1671	498	987	1710	1934	2474	1987	3368	716	776	837	1042	1305	1360	1539	1714	1777	2062	3146	3426	3426	3442	3504
Query Match	97.3	91.5	6.06	52.1	52.1		34.6	33.4	•	11.3		9.0				4.1	4.1	4.1	2.1	•	-	•	•	•	•			<u>.</u> -	1.0			1.9	•	1.9	1.9	1.9	1.9			1.9	1.9	1.9
Score	2114	1988	1974	1132	1132	908	752	126	126	245	2000	503	150	150	88	88	88	88				44	44	43	43	43		7.5	42	42	42	42	42	42	42	42	42	42	42	42	42	42
Result No.	1,	3 E	4	S	9	-	œ (	ص	01:	11	7 1	14	15	16	11	18	19	50	21	22	23	24	52	76	27	87.		ი გ ⊱	32	33	34	35	36	33	38	39	40	41	42	43	44	45

ALI GNMENTS

gpl00=melanocyte lineage-specific antigen/Pmell7 homolog [human, mRNA, 2130 nt]. 25-JAN-1995 mRNA 2130 bp S73003 DEFINITION

RESULT

g639589 ACCESSION

NID KEYWORDS SOURCE

human. ORGANISM

Homo sapiens

Aug 27 08:56 US-08-231-565A-26.rgc		Db 431 cttgccatctggctcttggtctcagaagagaagctttgtttatgtctggaagacctggg 490	Db 491 gccaatactggcaagttctagggggcccagtgtctgggctgagcattgggacaggcagg	Db 551 caatgctgggcacacacacatggaagtgactgtctaccatcgccggggatcccggagct 610	Db 611 atgtgcctcttgctcattccagctcagccttcaccattactgaccaggtgcctttctccg 670	Db 671 tgagcgtgtcccagttgcgggccttggafggagggacaagcacttcctgagaaatcagc 730	Db 731 ctctgacctttgcctccagctccatgaccccattggctatctggctgaagctgacctt 790	Db 791 cctacacctgggactttggagacagtagtggaaccctgatctcgggcacttgtggtca 850	Db 851 ctcatacttacctggagcctggcccagtcactgcccaggtggtcctgcaggctgccattc 910	Db 911 ctctcacctcctgtggctcctcccagttccaggcaccacagatgggcacaggccaactg 970	Db 971 cagaggccctaacaccacagctggccaagtgcctactacagaagttgtgggtactacac 1030	Db 1031 ctggtcaggcgccaactgcagagccctctggaaccacatctgtgcaggtgccaacactg 1090	Db 1091 aagtcataagcactgcacctgtgcagatgccaactgcagagagcacaggtatgacacctg 1150	Db 1151 agaagtgccagtttcagagtcatgggtaccacactggcagagatgtcaactccagagg 1210	Db 1211 ctacaggtatgacacctgcagaggtatcaattgtggtgctttctggaaccacagctgcac 1270	Db 1271 aggtaacaactacagagtgggtggagaccacagctagagagctaccctgagcctg 1330 	Db 1331 aaggtecagatgecageteaateatgtetaeggaaagtattaeaggtteeetgggeeeec 1390
Aug 27 08:56 US-08:231:565A-26.rgc 3	d. to 2130)	Adema, Jour., de Boef, A.J., Voder, A.B., Loenen, A.B. and rayou, V. Molecular characterization of the melanocyte lineage-specific antigen gp100 J. Biol. Chem. 269 (31), 20126-20133 (1994)	REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 154938] from the original journal article.  COMMENT NCBI gi: 639589 FEATURES Location/Qualifiers		/note="melanocyte lineage-specific antigen/Pmell/ homolog; melanoma marker protein. Method: conceptual translation supplied by author. NCBI gi: 639590" /codon.start=1	/product="gp100" /db_xref="PID:g639590" /tranglation="MDIVIARCLHHAVIGALIAVGATKVPRNQDWIGVSRQIRTKAW NRQLYPEWTTAQRLDORRGGQVSIKVSNDPPTJIGANASFSIAINFPGSQKVIPDGQV	IWONTI I NGSQWGGQPVTPQETDDACIEDDGEPCESGWSQRASFY TYDQYFGYY QVLGGPVSGLSI GYGRAMCITTMECYTYHRRGSRSYPPLABSSAFTI TYDQYFESVS VSQ.BRA.DGGWKHPLRNQPLTFALQLDPSCYLAEADLISTYMDFGDSSGTLISBALVY THTYLEPGPVTAQVVLQAAI PLTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVG	TYPCOARTARPSCTTSNOVPTTENTSTAPNOMPTAESTGMYPEKNYPNSENGEN STPEATCMTPAEVINVISCTTAAQNTTTENVETTARELE IPEPECEDASSIMSTESI TGSLGPLLDGTATLRUKRQVPLOVPLOCYPTRARELE IPEPECEDASSIMSTESI ARELITYSCQCELPKEACMEI SSPCQPPAQRILQPVLPSPACQULHQTIKGGSGTYC ARELITYSCA ANTWOLA I AUTOCARAT CHITTAIN MANTARI AST IVODI MOON	LANDALINALAND Y ALLIBE CAGARACACAN PLATA CALLAN VILADA MANUN LANDALINALANDO FEVINOLETE SENDENCE PLATA CALLANDO FERONOLETE COUNT 484 a 587 c 484 t CALLANDO FERONOLETE COUNT 486 A 587 C 587 C 681 C 68	Query Match 97.3%; Score 2114; DB 59; Length 2130; Best Local Similarity 99.9%; Pred. No. 0.00e+00; Matches 2117; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	<pre>Db 11 ggaagaacacaatggatctggtgctaaaaagatgccttcttcatttggctgtgataggtg 70                                     </pre>	Db 71 ctttgctggctgtgggggctacaaaagtacccagaaaccaggactggcttggtgtctcaa 130  {}	Db 131 ggcaactcagaaccaaagcctggaacaggcagctgtatccagagtggacagaagcccaga 190 	Db 191 gacttgactgctggagaggtggtcaagtgtccctcaaggtcagtaatgatgggcctacac 250 	Db 251 tgattggtgcaaatgcctcctctctattgccttgaacttccctggaagccaaaaggtat 310	Db 311 tgccagatgggcaggttatctgggtcaacaataccatcatcaatgggagcaggtgtggg 370 	Db 371 gaggacagccagtgtatccccaggaaactgacgatgcctgcatcttccctgatggtggac 430

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15-JUN-1990

Human 95 kD melanocyte-specific secreted glycoprotein mRNA, 3'

2114 bp

HUMGPMSS

LOCUS DEFINITION

g183559 M32295

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melanocyte-specific secreted glycoprotein. Human melanoma cell line, cDNA to mRNA, clone

Homo sapiens

ORGANISM NID KEYWORDS SOURCE ACCESSION

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δ	1828	GCTGATCGTGGGCATCTTGCTGGTGTGGTGGTGCTTGCATCTCTGATATATA 1	887
Ор	1871	ggcgcagacttatgaagcaagacttctccgtaccccagttgccacatagcagcagtcact 19	930
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BASE COUNT ORIGIN

 RESULT 4
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 LOCUS
 HUMPMEL
 2131 bp
 mRNA
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 DEFINITION
 Human Pmel 17 mRNA, complete cds.
 ACCESSION
 M77348

 NID
 91910105
 FM1910105

 KEYWORDS
 Pmel 17 protein; melanocyte.

 SOURCE
 Homo sapiens skin cDNA to mRNA.

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epithelium 08-MAR-1993 Bovinae; Theria; pigment Chordata; Vertebrata; Mammalia; Bovidae; retinal MAM end. Eutheria; Artiodactyla; Ruminantia; Pecora; 'n calf mRNA, æ (RPE1) Unizap 1584 bp al pigment ( (library: Eukaryota; Animalia; (bases 1 to 1584) retinal pigment. Bovine retinal M81193 CDNA to mRNA. Bos taurus Bos taurus BOVBRPEIA g162770 Bovini DEFINITION ORGANISM REFERENCE ACCESSION KEYWORDS SOURCE LOCUS NID

RESULT

Kim, R.Y. and Wistow, G.J.

AUTHORS

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/trānslation="QYmQVLGGPVSGLSIGTDKAMLGTYNMEVTVYHRRGSQSYVPLA HSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTFALQLHDPSGYLAGADLSYT EAPCTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVGTTPEQVATSKVLSTT VVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTPEPAGSNTSSFMPT EGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIVSIESAEILQAVSSSE GDAFELTVSCOGGLPKEACMDISSPGCOLPAQRICQPVPPSPACQIVILHQVIKGGSGT YCLAVSLADANSLAMVSTQLVMPQQEAGLRQAPLFVGILLVITAILLIASLIYRRRIMK QGSEVPLPQLPHGRTQWIRLPMVFRSCPIGESKPLLSGQQV" WDFGDSTGTLISRALTVTHTYLESGPVTAQVVIQAAIPLTSCGSSPVPGTTDRHVTTA 21; and monoclonal antibody HMB-50 define gene products 568 aatgetgggcacatataacatggaagtgactgtetaccaccgccgggggteccagageta 120 628 180 688 240 748 300 ctacacctgggactttggtgacagtacagggaccctgatctctcggggcactcacggtcac 360 CTACACCTGGGACTTTGGAGACAGTAGTGGAACCCTGATCTCTCGGGCACTTGTGGTCAC 868 420 928 480 9 Gaps tetgacetttgecetecagetecatgateceagtggetatttggetgggggtgacettte 569 AATGCTGGGCACACACACCATGGAAGTGACTGTCTACCATCGCCGGGGATCCCGGAGCTA gagtgtgtctcagctgcaggccttggatggaaggaacaagcgcttcctgagaaagcagcc teteacetectgtggetectetecagttecaggeactacagataggeatgtgacaactge 52; preferentially expressed in retinal pigment epithelium Curr. Eye Res. 55, 657-662 (1992) Length 1584; /dev\_stage="calf" /sequenced\_mol="cDNA to mRNA" /tissue type="retinal pigment epithelium" /tissue\_lib="Unizap XR" Indels 0; Mismatches 230; 37.1%; Score 806; DB 33; 82.7%; Pred. No. 0.00e+00; /note="ORF; NCBI gi: 162771" piqment" organism="Bos taurus" /db xref="PID:g162771 Location/Qualifiers 5 /product="retinal 418 /codon start=2 /gene="RPE1" 473 c Conservative partial/ 1..1584 NCBI gi: 162770 CDNA RPE1 Similarity 340 Matches 1348; The Query Match Local source COUNT 241 19 689 809 869 121 629 301 361 JOURNAL 181 421 CDS FEATURES TITLE COMMENT ORIGIN BASE 염 염 유 g G g ð à δ g à 유 δ 8 ò ð

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ö Gaps ö Length 1881; 0; Mismatches 198; Indels Score 752; DB 61; Pred. No. 0.00e+00; tch 34.6%; al Similarity 82.8%; 950; Conservative Query Match Local Matches

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exons 4,5, Version dene, BP. 2001 Last updated, Human melanocyte protein Pmel 17 DNA; PRI; 23-DEC-1995 (Rel. 46, Created) 23-DEC-1995 (Rel. 46, Last upd standard; Homo sapiens (human) HSMET03 U31797; RESULT ID HS

and

human Mammalia; Hominidae. the (Pmel 17), Vertebrata; Catarrhini; "Genomic organization and sequence of D12S53E homologue of the mouse silver (si) locus"; Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini; Bailin T., Lee S.T., Spritz R.A.; 1 - 2001

Unpublished.

1 - 2001

Mall, University Submitted (17-JUL-1995) to the EMBL/GenBank/DDBJ databases. Richard A. Spritz, Medical Genetics, 445 Henry Mall, Univer Wisconsin, Madison, WI 53706, USA. Location/Qualifiers Bailin T.;

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/map="12q13-q14" /note="DSEG number: D12S53E" sapiens' /organism="Homo ( source

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話話		RESULT LOCUS	10 HSPMEL03
담담	/number=5 exon 10301755	DEFINITION ACCESSION	
E 8	/number=6 Sequence 2001 BP; 457 A; 554 C; 492 G; 498 T; 0 other;	NID KEYWORDS	g1120059 ; <sub>ef E</sub>
ဝ်∺ို ဦး	Query Match 33.4%; Score 726; DB 10; Length 2001; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SECMENT SOURCE ORGANISM	
a B	1030 gaccaggtgcctttctccgtgagcgtgtcccagttgcgggccttggatgga	REFERENCE AUTHORS TITIE	Vertebra Vertebra E 1 (base S Bailin, T Genomic
a 6		JOURNAL REFERENCE	
를 함 로	ctggctgaagctgacctctcctacacctgggactttggagacagtagtggaaccctgatc	TITLE	
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Db Qy	1330 gatgggcacaggccaactgcagaggcccctaacacacagctggccaagtgcctactaca 1389 	exon	
අු	1390 gaagttdtgggtactacacctggtcaggcgccaactgcagagccctctggaaccacatct 1449	BASE COUNT ORIGIN	154 TN
δ	1029 GAACTTGTGGGTACTACACCTGGTCAGGCGCCAACTGCAGAGCCCTTGGAACCTCT 1088	Query Match	Match
q	1450 gtgcaggtgccaaccactgaagtcataagcactgcactg	Best Lo Matches	best Local Similar Matches 726; Co
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٥y	1149 AGCACAGGTATGACACCTGAGAAGGTGCCAGTTTCAGAGGTCATGGGTACCACACTGGGA 1208	Db 109	1090 cacttcctga
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В	1690 ctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacggaaagtatt 1749	Qy 84	849 TCTCGGGCAC
ý	1329 CTACCTATCCCTGAGCCTGAAGGTCCAGATGCCAGCTCAATCATGTCTACGGAAAGTATT 1388	Db 1270	0 gtcctgcagg
Op	1750 acaggt 1755	0й 909	
δ	1389 ACAGGT 1394	Db 133	1330 gatgggcaca

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DEFI	DEFINITION	Human melanocyte protein Pmel 17 gene, exons 4,5, and 6.
NID	TO TOO	g1125059
KEY	KEYWORDS	
SECMENT	ENT	3 of 5
SOURCE	URCE	human.
Ď	MCT NTO	nomo saprems Rukarvotas: mitochondrial sukarvotes: Metazoa: Chordata:
		Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo.
REFE	REFERENCE	
AU	AUTHORS	(Pmel 17)
1	1	2000
OC OC	JOURNAL	Unpublished (1995)
REFE	REFERENCE	2 (bases 1 to 2001)
AU	THORS	Bailin, T.
11	TOTIONAL	1995) Biohard & Garitz Medical Canal
5	TUNNO	of Wisconsin, Madison, WT 53706, USA
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dy 969 gategecacageccaactecagageccctaacaccacagecgeccaactecctactaca 1028	Db 1390 gaagttgtggtactacacctggtcaggcgaactgcagacctctggaaccacatct 1449 	<pre>Db 1450 gtgcaggtgccaaccactgaagtcataagcactgcacctgtgcagatgccaactgcagag 1509                                     </pre>	Db 1510 agcacaggtatgacacctgagaaggtgccagtttcagaggtcatgggtaccacactggca 1569 	Db 1570 gagatgicaactccagaggctacaggiatgacacctgcagaggiatcaatigiggigcti 1629 	Db 1630 tctggaaccacagctgcacaggtaacaactacagagtggagaccacagctagaga 1689 	Db 1690 ctacctatcctgagctgaaggtccagatgccagctcaatcatgtctacggaaagtatt 1749 		QY 1389 ACAGGI 1394 RESULT 11 TO USURIOS Abandand, MWA, DDI, 1170 DD	U31799, 23-DEC-1995 (Rel. 46, Created) 23-DEC-1995 (Rel. 46, Last updated, Human melanocyte protein Pmel 17 gen		RN [1] RP 1-1178 RA Bailin T., Lee S.T., Spritz R.A.; RT "Genomic organization and sequence of D12553E (Pmel 17), the human RT monso of the monso giver (gi) logis".	Unpublished. [2] 1-1178		The first officers, for the first officers of the fey for the fer	FT source 11178 //organism="Homo sapiens" //organism="12" //map="12q13-q14" //map="12q13-q14" //note="DSEG number: D12553E" FT //note="DSEG number: D12553E" FT //note="DSEG number: D12553E"  FT // CDS join(U31808:158232,U31807:128241,U31807:400546,U3179

736..821, U31798:932..1135, U31798:1238..1327, 298..43 t="melanocyte protein Pmel 17" sf="PID:q1125063" stion="MDLVIKRCLIHLAVIGALIAVGATKVPRNQDWLGVSRQLRTKAW 9, U31797: 623..781, U31797: 1030..1755, U31798: 382..496 QVVIQAA IP LTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQ ITEAQRLD CWRGGQVSLKVSNDGPTLIGANASFSIALNFPGSQKVLPDGQVI IGSQVWGGQPVYPQETDDAC1FPDGGPCPSGSWSQKRSFVYVWKTWGQYWQV SIGTGRAMLGTHTMEVTVYHRRGSRSYVPLAHSSSAFTITDQVPFSVSVSQ STTSVQVP TTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEAT IVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSLGPL ALVKRQVP LDCVLYRYGSFSVTLDIVQGIESAEILQAVPSGEGDAFELTVSC CMEISSP GCQPPAQRLCQPVLPSPACQLVLHQI1KGGSGTYCLNVSLADTN !LIMPGQEAGLGQVPLIVGILLVLMAVVLASLIYRRLMKQDFSVPQLPHSS KHFLRNQPLTFALQLHDPSGYLAEADLSYTWDFGDSSGTLISRALVVTHTY ö atettetgetettgteccattggtgagaatageccetecte 414 Gaps ; 0 Length 1178; Indels NIFCSCPIGENSPLLSGQQV"
N; 231 C; 373 G; 276 T; 0 other; gp100; ME20; NCBI gi: 1125063" US-08-231-565A-26.rge 3%; Score 245; DB 10; I 6%; Pred. No. 3.61e-110; ve 0; Mismatches 1; start=1 Aug 27 08:56

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THTYLEPGFVTAQVVLQAAIPLTSGGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVG
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TGS LGP LLDGTATLRLWKRQVP LDCVLYRYGSFSVTLDIVQCIESAEILQAVPSGEGD
AFELTVSCQGGLPKEACMEISSPGCQPPAQRLCQPVLPSPACQLVLHQIIKGGSGTYC
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                                                                                                                                                                                Bailin,T., Lee,S.-T. and Spritz,R.A. Genomic organization and sequence of D12S53E (Pmel 17), the human homologue of the mouse silver (si) locus
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                                                                                                                                                                                                                                                                                                                      Submitted (17-JUL-1995) Richard A. Spritz, Medical Genetics, 445
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                                                                                                                                                                                                                                                                                                                                         Henry Mall, University of Wisconsin, Madison, WI 53706, USA
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Bailin, T., Lee, S.-T. and Spritz, R.A. Genomic organization and sequence of D12S53E (Pmel 17), the human Direct Submission Submitted (17-JUL-1995) Richard A. Spritz, Medical Genetics, 445 Henry Mall, University of Wisconsin, Madison, WI 53706, USA NCBI gi: 1125060 ö 1050 agggtggctcggggacatactgcctcaatgtgtctctggctgataccaacagcctggcag 1109 Human melanocyte protein Pmel 17 gene, exons 7, 8, 9, and 10. Gaps Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 930 ggctgcccaaggaagcctgcatggagatctcatcgccagggtgccagcccctgcccagc Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 0, Length 1559; Indels homologue of the mouse silver (si) locus Score 209; DB 86; Pred. No. 1.98e-90; /note="DSEG number: D12S53E" 414 t 0; Mismatches /organism="Homo sapiens" tggtcagcacccagcttatcatgcctggt 1138 Location/Qualifiers 1..1559 413 g /chromosome="12" /map="12q13-q14" 1559 bp (bases 1 to 1559) (bases 1 to 1559) /number=10 Query Match 9.6%; Best Local Similarity 100.0%; 1238..1327 Unpublished (1995) 209; Conservative /number=7 /number=8 932..1135 /number=9 382..496 736..821 Homo sapiens 2127 AGCCTGA 2133

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1 (bases i to 673)
Bailin,T., Lee,S.-T. and Spritz,R.A.
Genomic organization and sequence of D1253E (Pmel 17), the human homologue of the mouse silver (si) locus ö Submitted (17-JUL-1995) Richard A. Spritz, Medical Genetics, 445 224 AGCIGGICAAACTGTCCCTCAAGGTCAGTAATGATGGGCCTACACTGATTGGTGCAAATGC 283 396 aggtggtcaagtgtcctcaaggtcagtaatgatgggcctacactgattggtgcaaatgc 455 19-DEC-1995 Gaps Eukaryotae; mitochondrial eukaryotee; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Henry Mall, University of Wisconsin, Madison, WI 53706, USA NCBI qi: 1125058 456 ctecttetetattgeettgaactteeetggaageeaaaaggtattgeeagatgggeaggt ; 0 Human melanocyte protein Pmel 17 gene, exons 2 and 3. Length 673; 0; Indels Score 150; DB 86; Pred. No. 1.46e-58; 0; Mismatches /map="12q13-q14" /note="DSEG number: D12S53E" 166 /organism="Homo sapiens"/chromosome="12" 516 tatctgggtcaacaataccatcatcaatgg 545 Location/Qualifiers 179 g 673 bp Query Match 6.9%; Best Local Similarity 100.0%; 142 c (bases 1 to 673) Matches 150; Conservative /number=3 /number=2 Unpublished (1995) Direct Submission 128..241 400..546 15 RESULT

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm

MPsrch nn

Tue Aug 27 09:09:30 1996; MasPar time 177.89 Seconds 868.381 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-231-565A-26 (1-2172) from US08231565A.seq 2172 Description: Perfect Score:

N.A. Sequence:

Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 91712 seqs, 35561689 bases x 2 Searched:

Post-processing: Minimum Match 0%

Listing first 45 summaries

n-geneseq23

Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17

Mean 9.903; Variance 7.604; scale 1.302 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	0.00e+00	0.00e+00	0.00e+00	2.95e-29		2.36e-08		1.88e-07	1.88e-07
Description	MART-1 melanoma antig	Sequence encoding mel	Melanoma-specific imm	Human Natriuretic Pep	Human Natriuretic Pep	Rat SIII 15 kDa subun	Base substituted E.co	Rat allograft inflamm	Rabbit zona pellucida
<b>a</b>	T02716	096055	T03760	010572	010572	990525	N81164	099380	065607
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Query Match Length DB	2172 17	2115	2131	1047	1047	458	204	350	1338
Query Match	100.0	96.7	90.7	4.1	4.0	2.1	2.0	2.0	2.0
Score	2112	2101	1970	88	98	45	44	43	43
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t 6.69e-08 1 1.88e-07	ŗ,	5.27e-	1.46e-	1.46e-	5.27e-	1.46e - 06	1.46e-06	1.46e - 06	1.4	1.46e-06	~	7	2	S	c 1.46e-06	_	-	_		•		•	4.	4.		4.	4.	4.	4.	4	•	.04e-0	4	t 4.04e-06
Rape acyl-ACP thioest Human ubiquitous nucl	Oligonucleotide probe	Oligonucleotide probe	Human superoxide dism	Rape abscission/dehis	Thrombopoietin coding	RP-8 Programmed cell	Cyclin D1 gene.	Human cyclin D1.	Placenta-specific pro	mPD-1 cDNA.	Murine programmed cel	Human pro-urokinase	Human c-myc far upstr	Human c-myc far upstr	inase	Plasmid pAU157 sequen	Plasmid pAU157 insert	Sequence of plasmid p	-	Clone Imd2 encoding	Murine glycosylation	Hybrid human/pig SOD	Human SOD.	P14(T) allergen clone	Fragment of plasmid p	CAD cDNA isolated fro	Human anti-HBs heavy	Tomato acid invertase	Human heregulin-beta2	Full-length foetal hu	18-	pMx34 cDNA insert.		p150.95 alpha subunit
Q47966 Q88760	051746	051746	058663	073729	099552	973760	031873	053197	005879	095309	055770	020360	068910	606890	204107	N60889	60609N	N60864	Q11712	005304	075445	061575	961572	022352	005160	Q38027	049944	063892	Q31546	048393	014263	N71034	N60848	890900
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2.0	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8
44	42	42	41	41	42	41	41	41	41	41	41	41	42	42	41	41	41	41	41	42	40	40	40	40	40	40	40	40	40	40	40	40	40	40
110	12	13	14	15	16	11	18	19	70	21	22	23	24	52	56	27	58	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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#### ALIGNMENTS

RESULT 1		•	DT 20-APR-1996 (first entry)	DE MART-1 melanoma antigen cDNA25.	KW cDNA25; MART-1; melanoma antigen recognised by T-cells;	-	W tumour-associated antigen; immunogen; diagnosis; prognosis;	W prophylaxis; therapy; vaccine; ds.	Mammalian.	Key	T CDS 382038		T /note= "cDNA25 melanoma antigen"	N W09529193-A2.	D 02-Nov-1995.		•						T DNA encoding melanoma antigens recognised by T-lymphocytes - also	
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Vectors, host cells and antibodies, used to detect, treat and immunise animal against melanoma.  Disclosure; Fig 4A-4B; 184pp; English.  The nucleic acid encodes CDNA25, a melanoma antigen (WART-1)  Which is recognized by T-lymphocytes. cDNA25 is a derivative of the melanocyte-melanoma-specific antigen gpl00 (see R84855).  Antigen cDNA25 is a source of immunogenic peptides (see R84199) which are optionally modified (see R84200-R84211) and used in medicaments, especially vaccines, for the treatment or prevention (by immunization) of melanoma. Antibodies against cDNA25 and its immunogenic peptides may be used in the detection and isolation of the antigen from a sample, the detection of which is indicative of a disease state (melanoma or metastatic melanoma).  Sequence 2172 BP; 512 A; 594 C; 578 G; 488 T;	Query Match 100.0%; Score 2172; DB 17; Length 2172; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 2172; Conservative 0; Mismatches 0; Indels 0; Gaps	ccaatcgcgaccgggaagaacacaatggatctggtgctaaaagat 6 	gccttcttcatttggctgtgataggtgctttgctggctgtggggctacaaaagtacca 12 	gaaaccaggactggcttggtgtctcaaggcaactcagaaccaaagcctggaacaggcagc 18 	tgtatccagagtggacagaagcccagagacttgactgctggagaggtggtcaagtgtcc 24( 	tcaaggtcagtaatgatgggcctacactgattggtgcaaatgcctccttctctattgct 30 	tgaacttcoctggaagccaaaaggtattgccagatgggcaggttatctgggtcaacaata 36 	ccatcatcatgggagccaggtgtggggaggacagccaftgtatccccaggaaactgacg 42 	atycctgcatcttccctgatgtggaccttgccatctggctcttggtctcagaagagaa 48 	gctttgtttatgtctggaagacctggggcaatactggcaattctagggggccagtgt 540 	ctgggctgagcattgggacaggcagggcaatgctgggcacacaca	totaccatogcogggatocoggagotatgtgcotottgctcattocagotoagocttoa 66 	${\sf ccattactgaccaggtgcctttctccgtgagcgtgtcccagttgcgggccttggatgga$
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<u>6</u>	61 GCACCACAGATGGGCACAGGCCAACTGCAGGGCCCCTAACACCACAGGGCCCAAGTG	1020
10	021 ctactacagaagttgtgggtactacacctggtcaggcgccaactgcagagccctctggaa	1080
100	21 CTACTACAGAAGTTGTGGGTACTACACCTGGTCAGGCGCCCAACTGCAGAGCCCTTTG	1080
10	081 ccacatctgtgcaggtgccaaccactgaagtcataagcactgcacctgtgcagatgccaa	1140
100	81 CCACATCTGTGCAGGTGCCAACCACTGAAGTCATAAGCACTGCACCTGTGCAGATGCC	1140
117	41	1200
117	41 CTGCAGAGAGCACAGGTATGACACCTGAGAAGGTGCCAGTTTCAGAGGTCATGGGTACC	1200
12(	01 cactggcagatgtcaactccagaggctacaggtatgacacctgcagaggt	1260
12(	01 CACTGGCAGAGATGTCAACTCCAGAGGCTACAGGTATGACACCTGCAGAGGTATCAATT	1260
12	61 tggtgcttctggaaccacagctgcacaggtaacaactacagagtgggtgg	1320
	61 TGGTGCTTTCTGGAACCACAGCTGCACAGGTAACAACTACAGAGTGGGTGG	1320
133	2	1380
133	21 CTAGAGAGCTACCTATCCCTGAGCTCGAGGTCCAGATGCCAGCTCAATCATGTCTACG	1380
136	81 aaagtattacaggttccctgggccccctgctggatggtacagccaccttaaggctggt	1440
13(	381 AAAGTATTACAGGTTCCCTGGGCCCCTGCTGGTTACGTACAGCCACCTTAAGGCTGGTGA	1440
144	41 agagacaagtcccctggattgtgttctgtatcgatatggttcctttccgtcaccc	1500
144	41 AGAGACAAGTCCCCCTGGATTGTGTTCTGTATGGTATGG	1500
15(	01 acattgtccagggtattgaaagtgccgagatcctgcaggctgtgccgtccggtga	1560
15(	01 ACATIGICCAGGGTATTGAAAGTGCCGAGATCCTGCAGGCTGTGCCGTCCGGTGAGGG	1560
15(	61 atgcatttgagctgactgtgtcctgccaaggcgg	1620
15(	61 AIGCATITGAGCIGACIGTGICCIGCCAAGGGGGGCIGCCCAAGGAAGCCIGCAIGGA	1620
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අ ද	611 atgtgcctcttgctcattccagctcagccttcaccattactgaccaggtgccttctccg 6/0	13/1 aaggegggeegeecaaggaageetgeatgaageetearegeeagggggggggeereegeegeegeereegeereegeereegeereegeereegeereegeereegeereegeereegeereegeeg
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γ	748 CTCTGACCTTGCCCTCCAGCTCCATGACCCCAGTGGCTATCTGGCTGAGCTGACCTCT 807	1708
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ŝ	CIVICACCICCIGIGOCCCCAGIICCAGGCACCACAGAIGGGGAACAGGCCAACIG 307	
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Ž	CIGAI(AOGCOCCAACIGCAGGCCCICIGGAACCACAICIGGCAGGGCCAAACCACIG IIO)	
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96 A	151 agaaggtgccagtttcagaggtcatgggtaccacactggcagagatgtcaactccagagg	2111 gcctg 2115        2128 GCCTG 2132
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δy	1408 TCTCGGATGGTACACCCACCTTAAGGCTGGTGAAGAGACAAGTCCCCCTGGATTGTGTTC 1467	
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δ	1468 TGTAICGATAGGTTCCTTTTCCGTCACCTGGACATTGTCCAGGGTAITGAAAGTGCCG 1527	phel.17 - are highly potent stimulators of HLA-A2+CTL's useful in

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δ d	1708	TACTGAAGGGTGGCTCGCGGGAATACTGCCTCAATGTGTCTCTGGCTGATACCAACAGCC 1767
g &	1741	tggragrggcragaeccragettatcatcatgcetgggattetteteccracaggread 1000
q <sub>0</sub>	1801	aagcaggccttgggcaggttcggctgatcgtgggcatcttgctggtgttgatggctgtgg 1860
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g	1921	tgccacatagcagcagtcactggctgggtctaccccgaatcttctgctcttgtccattg 1980
Š	1927	TGCCACATAGCAGCAGCACTGGGTGGGTTGCTTCTTGTTGTTTGT
g	1981	gtgagaatagcccctcctcagtggcagcaggtctgagtactctcatatgatgctgtga 2040
δ	1987	GIGAGAACAGCCCCCTCCTCAGTGGGCAGGTCTGAGTACTCTCATATGATGCTGTGA 2046
g	2041	ttttcctggagttgacagaacacctatatttccccagtcttccctgggagactactat 2100
δ	2047	TTTCCTGGAGTTGACAGAAACACCTATATTTCCCCCAGTCTTCCCTGGGAGACTACTAT 2106
В	2101	taactgaaataatactcagagcctgaaaaa 2131
λo	2107	TAACTGAAATAATACTCAGAGCCTGAAAA 2137
50	ULT Q1057	LT 4 Q10572 standard; DNA; 1047 BP.
N S	01057 09-AE	2; R-1991 (first entry)
H 25	Humar NPRB;	retic Peptide Receptor B.
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표표	Key Peptide	Location/Qualifiers de 122
55	/label= Protein	signal s
5 5	/labe	L mature NPBR
: = :	/label	extracellular domain
크	/note= Domain	"binds natriuretic peptides A,B and CJ 456456
FI	/label= Domain	.l= transmembrane domain n 4791047
E 5	/labe	cytoplas
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δy	: : : : :       : :         : :
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ζ	1553 TGAGGGGATGCATTTGAGCTGACTGTGTGCCGAAGGCGGGCTGCCCAAGGAAGCCTG 1612
a	627 nvkgmannhnsnnsshgsnkssncvvdsrnvnkntdygnasnretannddnnanyakknn 686
δy	1613 CATGGAGATCTCATCGCCAGGGTGCCAGCCCC-CTGCCCAGCTGTGCCAGCCTGTGC 1671
q	687 tannnnsgnnnnttgmnaadvysngnnnnnnanrsgnnynngndnsnknnvnkvrngnrn 746
à	
ą	747 ynrnsndrtnnnnnvnnmnrcwandnanrndngnnkgnnrrnnknggtsnndnnnrmn 806
ć	1732 ACTGCCTCAATGTCTCTGGCTGATACCAACAGCCTGGGGTCAGCACCCAGCTTA 1791
ą	807 nyannnnknvnnrtnaynnnkrkanannynnnnhevannnkrgntvnanandsvtnynsd 866
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RESULT	1.17 5 0.105.73 ch. 2.4. D.
2 2	210572;
Į.	09-APR-1991 (first entry)
出逐	Human Natriuretic Peptide Receptor B. NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
æ S	hyperaldosteronism; glaucoma; guanyl cyclase. Homo sapiens.
표	
H	Peptide 127 /label= signal sequence
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E E	/label= mature NPBR Domain 23455
<u>.</u>	= extracellular domain
H	/note= "binds natriuretic peptides A,B and C]"
	= transmem
<u> </u>	Domain 4791047 //abel= cytoplasmic domain
1 5	/note= "GC and protion kinase activity"
E	Modified -site 2426
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kinase activity. The DNA can be inserved and mutated to produce for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of moly the protein (or variants) can be used to treatment of the protein (or variants) can be used in treatment of the protein (or variants) can be used in treatment of the protein (or variants) can be used in the protein of t The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English. h 4.0%; Score 86; DB 2; Length 1047; Similarity 9.5%; Pred. No. 3.04e-28; 92; Conservative 279; Mismatches 581; Indels 15; 51 T; 83 G; 15 C; 87 A; ä Query Match
Best Local Similarity 9.5%; /label= N-qlycos\_site W09100292-A. 10-JAN-1991. 22-UN-1999, U03586. 23-UUN-1999, US-370673. (GETH) GENENTECH INC. Chang M, Goeddel D, Lowe D; WPI; 91-036711/05. N-PSDB; Q10324. Modified -site 277..279 /label= N-glycos\_site Modified -site 244..246 /label= N-glycos site Modified -site 600..602 /label= N-glycos site Modified -site 349..351 Modified -site 195..197 /label= N-glycos\_site also be prepd. Matches THE FET THE FE

Gaps 15; 1498 AGGTGACGGAAAAGGAACCATATCGATACAGAACACAATCCAGGGGGACTTGTCTTTC 1439 1438 ACCAGCCTTAAGGTGGCTGTACCATCCAGCGGGGGCCCCAGGGAACCTTTCC 1379 : | | : :|: :: | : :|1318 GTAGACTTGAGGCTTCAGGCTTCAGGCTTAGGGTAGCTCTCTTCTAGCT 1319 42 wnrvgnavanavnangrannvdnrnvssnnngacsnynannsavdnknyhdndnnngngc 101 102 vynaasvarnashwrnnnntagavasgns-akndhyrtnvrtgn-sankngnnvvtnhgh 159 160 nnwtaraannyndartddrnhyntnngvnnanngsnnsvnhnvyarnnggnnnathnnra 219 :: :: -: -: გ 음 쇰 გ. 임

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DP	757 nnnnnynnmnrcwandnanrndngnnkgnnrrnnkngqtenndnnnrmnnyannnnkny 816	. E.	RESULT <i>1</i> ID N81164 sta
ć		AC	N81164;
3.	לסן פריא-רופספטוראוופסא-פרופשמספטיעאטספוראאמספרופאווורוקשפעאטטור לס	日日	Base subst.
ηρ	817 nnrtnaynnnkrkanannynnnnhsvannnkrgntvnanandsvtnynsdnvgntansan 876	XX.	E.coli bet
ď		FH	Key
· 4	200 Annual Annual Control of the Standard Control of t	FT	misc_featu
9	8// stimmovytninadnytchaannangvykvitngaaymvssgniginginginannarmana 950	F	/function=
ç	AGAG	F	primer bin
Op	937 nndavssnrnrhrnhdnnrnrngvh-tgnvcagvvgnkmnrycnngdtvntasrmnsngn 995	PN	/*tag= D EP-285123-J
		PD	05-MAY-198
g,	00/ IGGIAGACAGICACIICCAIGGIGIGIGIGCCCAAGCAIIGCCCIGICCCAAIGCIC 340	7 K	03-APR-198
g	996 anknhvs 1002	PA	(suso) suo
g	547 AGCCCAG 541	DR	WPI; 88-27
•		PT	Introducin
RESULT		PT PT	by prepn o
12	Q90525 standard; cDNA; 458 BP.	PS	Disclosure
AC F	Q90525;	8 6	Random poi
5 점	oz-mov-1995 (iiist encig) Rat SIII 15 kDa subunit cDNA.	38	single str
X.	RNA-polymerase transcription factor SIII; ss.	88	it to gene
S H	Rattus sp. Kev Location/Oualifiers	38	possible n variable 3
FI		ည	reverse tr
E :	/*tag= a	ខ្ល	transcript
N G	EP-655498-A. 31-May-1005	8 5	The segment
PF	29-NOV-1994; 250286.	88	occurred a
PR.	30-NoV-1993; US-160087,	88	See also P
PI PI	(UNLAH-) UNLAHIOMA MED NES FOUND.  Bradsher JN, Conaway JW, Conaway RC;	Ž,	antanhac
R R	WPI; 95-195587/26, P-PSDB; R75086.	СΕЩ	Query Match Best Local Sin
PT	Novel RNA polymerase transcription factor SIII — useful for modulating the rate of transcription by RNA polymerase II.	24	Matches 33
PS	Claim 38; Page 18; 43pp; English.	QQ	34 bgcag
38	ITYPCIC peptides (given in Kiovau-so) of purilised fat sill pio subunit were used to design primers (Q90531-32) for the PCR	g	660 TGAAG
;		•	

Aug 27 09:00

tion of cDNA from a rat lambda-qt11 library. cDNAs the complete pl5 protein (R75086) were obtained by screening and brain lambda ZAP II cDNA libraries. 2 Overlapping clones

ined to generate the sequence given in Q90525. 458 BP; 186 A; 73 C; 85 G; 114 7

114 T;

. 0 Gaps .**.** Score 45; DB 15; Length 458; Pred. No. 2.36e-08; 0; Mismatches 11; Indels 2.1%; imilarity 83.6%; 6; Conservative

aaaa 447 |||| |AAA 2172

andard; DNA; 204 BP

ta galactosidase alpha-fragment; base substitutions; ss. 90 (first entry)
tituted E.coli beta-galactosidase alpha-fragment.

ia coli

Location/Qualifiers 19..69 ure

=multiple cloning site
nd 187..204

988; 105163. 987; US-034819. JOMEN SOKERI OY.

a P, Knowles J, Koivula A, Bamford J, Reinikainen T;

79927/40.

ng random point mutations into nucleic acods -of single stranded template, annealing a primer, elongation,

oration, completion of molecules and screening.

int mutations were introduced into the alpha fragment of ta-galactosidase. The wild type sequence was obtained as a randed template and an oligonucleotide was hybridised to e; p; English.

erate a popn of DNA molecules which terminate at all nucleotide positions within a specified region. The

3' ends generated in this way are used as primers for

ranscriptase. Nucleotides are misincorporated by the brase and the molecules are completed to forms that can be and then expressed in a suitable host-vector system. Early in any given mutant.

47 C; 17 G; 11 T; 108 Others; 204 BP; 21 A;

Gaps 2; Score 44; DB 1; Length 204; Pred. No. 6.69e-08; 65; Mismatches 57; Indels 2.0%; imilarity 21.0%; 3; Conservative

5;

ggycgacbcyrraggnycccggggywccgagcyc-gaayycdchvgccgymrttth 92 ||: || : ::|| | | ||::| |||:|| ::| :| :

ö fragments. The AIF-2 gene is a differentially expressed allograft gene fragments of this gene and/or the gene product are therefore useful in 93 hyrrmrbnvyrdynr-sdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnnc 151 Gaps which is expressed in allograft tissue during transplant rejection. Identification of the rat AIF-2 product (R80521) or transcript The diagnostic methods used allow rejection (vascular inflammation) to be detected at an early stage and require only a small amount of DNA encoding allograft rejection factors and immunogenic fragments 099372-099393 are rat allograft inflammatory factor 2 (AIF-2) cDNA indicates that allograft rejection is taking place. The rat AIF-2 given in sequence ID listing in the specification gives ; 0 AIF-2; allograft inflammatory factor 2; transplant rejection; Rabbit; lapine; zona pellucida; ZPC; immunocontraception; ds. Oryctolagus cuniculus. 0; Mismatches 10; Indels Rat allograft inflammatory factor 2 (AIF-2) cDNA fragment. 2.0%; Score 43; DB 16; Length 350; 129 T; useful for identifying transplant rejection inhibitors inhibitor; immunogenic; detection; diagnosis; ds Best Local Similarity 84.1%; Pred. No. 1.88e-07; 152 necebnnhvehnvhbnnhrnwayvrhdarrddvheev 188 540 ACACTGGGCCCCCTAGAATTGCCAGTATTGGCCCCA 504 63 G; Rabbit zona pellucida ZPC coding sequence. the diagnosis of transplant rejection. 37 C; Location/Qualifiers Claim 11; Page 92; 138pp; English. .T 9 Q65607 standard; cDNA; 1338 BP. Q99380 standard; cDNA; 350 BP. 121 A; 065607; 31-JAN-1995 (first entry) (first entry) 53; Conservative 17..1264 (HARD ) HARVARD COLLEGE. 21-DEC-1994; U14724. 21-DEC-1993; US-171385. Utans U; nucleotide 111 as C) Sequence 350 BP; :: :: WPI; 95-240668/31. biopsy material. Rattus sp. W09517506-A1. 2112 CAG 2110 08-FEB-1996 29-JUN-1995. Russell ME, 62 tag 64 Query Match 099380; Matches Key RESULT g ტ 쇰 g, ئ 요 염 음

ö A CDNA library was prepared from mRNA isolated from ovaries removed from 5 week old rabbits. The lambda gt10 library was screened with a porcine ZPC cDNA probe (Q65606). Two positive clones were sequenced and were found to be identical except that one contained 4 extra nucleotides at the 5'-end. The determined sequence was 75% Gaps ; 0 Use of zona pellucida proteins and antibodies - for inducing reproducible transient infertility or permanent sterility in 236 T; 2.0%; Score 43; DB 11; Length 1338; 8; Indels US-08-231-565A-26.mg 402 G; Best Local Similarity 86.4%; Pred. No. 1.88e-07; 0; Mismatches homologous to DNA coding for porcine ZPC. 445 C; Claim 22; Page 81-83; 154pp; English. Harris JD, Hsu KT, Podolski JS; 255 A; 51; Conservative 09-NOV-1992; US-973341. 29-JAN-1993; US-012990. (ZONA-) ZONAGEN INC. 06-NOV-1993; U10851. 1338 BP; WPI; 94-183156/22. female mammals P-PSDB; R55197 /product= 2PC WO9411019-A. 26-MAY-1994. Aug 27 09:00 Sequence Query Match Matches 쇰 δ 

Location/Qualifiers Q47966 standard; cDNA; 1710 BP. 25-MAR-1994 (first entry) 169..1269 Brassica napus. /\*tag= a 047966;

Claim 1; Figure 1; 48pp; English.
The nucleotide sequence is useful for transforming plant cells and altering that plants characteristics. Characteristics which may be altering that plants characteristics of a cyl-ACP thioseterase activity; (2) fatty acid yield and/or fatty acid composition and (3) yield and/or composition of seed storage oil. useful for transforming plants, for altering properties e.g. seed Rape acyl-ACP thioesterase (Clone pNL2) coding sequence. Enzyme precursor; acyl-ACP thioesterase; plant; transformation; fatty acid; yield; composition; seed oil; Brassica napus; ss. cDNA encoding enzyme with acyl-ACP-thio:esterase activity -Safford R, Slabas AR; /note= "Has acyl-ACP thioesterase activity." 337 C; /product= Enzyme precursor. Hellyer SA, Loader NM, WPI; 93-303472/38. P-PSDB; R41673. storage oil composition 16-SEP-1993. 03-MAR-1993; G00432. 03-MAR-1992; GB-004583. (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC. W09318158-A. 

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364 G;

534 A;

1710 BP;

Sequence

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Gaps

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24-MAY-1993; 108325

MK14 Oligonucleotide probe MK14A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Claim 3, Page 14, 23pp; English. Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but New oligo:nucleotide probes specific for Mycobacteria - used for New oligo:nucleotide probes specific for Mycobacteria - used for ; 0 ö 31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; cross reacted to a few non-mycobacterial spp. The probe may detection and amplification of Mycobacteria nucleic acid in detection and amplification of Mycobacteria nucleic acid in be useful as an initial screen for mycobacterial infection. See also 051735-45 and Q51747-59. 942 GGCTCCTCCCCAGTTCCAGGACCACAGATGGGCACAGGCCAACTGCAGG 991 11 ssvhsyyvvhvvshhhsvhhvvhhvhvhvhvhhvhyhvyvsv 60 10 gssvhsyyvvhvvshhhsvhhvvhhvhhvhvhvvhhvhvhhvhyhvyvs 59 4; Indels 4; Indels Score 42; DB 9; Length 91; Pred. No. 5.27e-07; 1.9%; Score 42; DB 9; Length 91; 4 T; Pred. No. 5.27e-07; 46; Mismatches 45; Mismatches 15 G; JT 14 Q58663 standard; cDNA to mRNA; 699 BP. 17 C; Claim 3; Page 14; 23pp; English. BP. 8 26-MAY-1992; US-889651. (BECT ) BECTON DICKINSON CO. 1.98; Query Match 1.9%; Best Local Similarity 0.0%; Best Local Similarity 2.0%; 5 A; 0; Conservative 1; Conservative 14-0CT-1994 (first entry) Q51746 standard; cDNA; 91 (BECT ) BECTON DICKINSON 26-MAY-1992; US-889651 Spears PA; Spears PA; 24-MAY-1993; 108325. WPI; 93-378844/48. 91 BP; WPI; 93-378844/48 EP-571911-A. 01-DEC-1993. Synthetic. Shank DD, Shank DD, Sequence Query Match samples sambles 058663; Matches Matches RESULT ID 05 AC 05 DT 14 염 염 ð გ ; 0 ö Gaps Gaps in detection, diagnosis and in screening assays for substances which diagnostic, drug design and therapeutic applications Claim 6; Page 148; 195pp; English. This genomic DNA isolated from human prostate cancer PC-3 cells may New ubiquitous nuclear receptor - used to develop prods, for use in hormone/retinoic acid receptor subfamily. The products can be used be expressed recombinantly to produce a UNRP which interacts with 8; Indels 0; ö the response elements and network of receptors in the thyroid Human ubiquitous nuclear receptor protein DNA. Ubiquitous nuclear receptor; drug design; disease diagnosis; 301 T; Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; Score 43; DB 15; Length 1813; Best Local Similarity 78.2%; Pred. No. 6.69e-08;
Matches 61; Conserustin interact with UNRPs for use in diagnosis, drug design and 529 G; Pred. No. 1.88e-07; 0; Mismatches 8; 573 C; Location/Qualifiers \_ = -= = = = 410 A; Q88760 standard; DNA; 1813 BP 31-MAY-1994 (first entry) Oligonucleotide probe MK14-A 1681 aaaaaaaaaaaaaaaa 1698 2155 AAAAAAAAAAAAAAA 2172 Q51746 standard; cDNA; 91 BP. 2.0%; Best Local Similarity 86.4%; 20-JAN-1996 (first entry) 51; Conservative therapeutic applications. 08-NOV-1994; U12883. 10-NOV-1993; US-152003. (ARCH-) ARCH DEV CORP. Sequence 1813 BP; Liao S, Song C; WPI; 95-194092/25. P-PSDB; R74738. W09513373-A1. Synthetic. EP-571911-A. 01-DEC-1993. Homo sapiens, therapy; ss. 18-MAY-1995.

Query Match

Matches

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051746;

ss. RESULT 055 ID 055 AC 055 DT 31-0 DE 01 DE 01 RW ss NW ss PN EPP PD 01 DD 01 DD

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Gaps

Human superoxide dismutase gene

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                                                                                                                                                                                                                                                       The sequence encodes a superoxide dismutase. The gene may be used to produce superoxide dismutase in increased yields by transforming it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or dehiscence, and can be used to manipulate plant abscission and reduce/prevent pod dehiscence, especially to regulate abscission of pollen from anthers, to generate male sterile plants and for hybrid
                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 3; 39pp; English.
The cDNA encodes a rape (cv. Rafal) protein involved in abscission
                                                                                                                                                                                                              DNA encoding human super:oxide dismutase (50D) and transformed microorganism - useful for prodn. of SOD Claim 1; Page 7; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant and isolated nucleic acids - encode enzymes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 T;
                                                                                                                                                                                                                                                                                               149 T;
                                                                                                                                                                                                                                                                                                                         Query Match 1.9%; Score 41; DB 10; Length 699;
Best Local Similarity 86.0%; Pred. No. 1.46e-06;
           Superoxide dismutase; SOD; transformation; production; ss.
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rape; pSAC51; abscission; dehiscence; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins involved in plant abscission or dehiscence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 6;
                                                                                                                                                                                                                                                                                                181 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rape abscission/dehiscence protein pSAC51 cDNA.
                                                                                                                                                                                                                                                                                               127 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 C;
                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coupe SA, Isaac PG, Roberts JA; WPI; 94-333203/41.
                                                                            /product= superoxide_dismutase
polyA_signal 625..699
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q73729 standard; cDNA; 756 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 A;
                                                                                                                                                                                                                                                                                               699 BP; 242 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NICK-) NICKERSON BIOCEM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "putative polyA site"
W09423043-A.
                                                                                                                                22-FEB-1994.
25-SEP-1992; 279193.
25-SEP-1992; JP-279193.
(NIPK ) NIPPON KAYAKU KK.
WPI; 94-097023/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                   49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633..638
                                                   68..529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15..458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-0CT-1994.
31-MAR-1994; G00689.
31-MAR-1993; GB-006726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crop improvement; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seed production.
Sequence 756 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica napus.
                                                                                                                                                                                                 P-PSDB; R47062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R60799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyA_signal
/*tag= b
                            Homo sapiens.
                                                                                            polyA_signal
                                                                                                                     J06046860-A.
                                                                                                                                                                                                                                                                                   into E.coli
                                                                  /*tag= a
                                                                                                                                                                                                                                                                                                 Sequence
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## US-08-231-565А-26 mg Aug 27 09:00

Gaps **;** Query Match 1.9%; Score 41; DB 12; Length 756; Best Local Similarity 97.7%; Pred. No. 1.46e-06; 1; Indels 0; Mismatches 42; Conservative Matches

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Search completed: Tue Aug 27 09:12:38 1996 Job time : 188 secs.

Aug 27 09:14

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn

Tue Aug 27 09:13:00 1996; MasPar time 847.32 Seconds 921.604 Million cell updates/sec Run on:

not generated. Tabular output

Description:

>US-08-231-565A-26 (1-2172) from US08231565A.seq 2172 Perfect Score:

N.A. Sequence: Comp:

Scoring table:

TABLE default Gap 6

514334 seqs, 179763086 bases x 2

Dbase 0; Query 0

STD:

Nmatch

Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

EST-STS Database:

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14

15:EST12 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST29 30:EST39 31:EST33 32:EST33 33:EST33 33:EST33 33:EST33 33:EST33 33:EST33 33:EST33 33:EST33 33:EST33 33:EST33 33:EST34 45:EST44 42:EST42 43:EST43 44:EST44 42:EST42 43:EST43 44:EST44 45:EST5 54:EST46 46:EST46 47:EST47 48:EST46 49:EST49 50:EST50 57:EST5 58:EST5 53:EST5 56:EST5 66:EST6 65:EST6 66:EST6 66:EST6 67:EST6 67:EST7 77:EST7 77:EST 77:EST

93:STS3 94:STS4 95:STS5 96:STS6 97:STS7

EST-STS-TWO

Database:

108:EST101 109:qnEST1 110:qnEST2 111:qnEST3 112:qnEST4 113:qnEST5 114:qnEST6 115:qnEST7 116:qnEST8 111:qnEST9 1119:qnEST9 1119:qnEST10 119:qnEST11 120:qnEST12 121:qnEST13 122:qnEST13 123:qnEST13 123:qnEST13 123:qnEST15 123:qnEST15 125:qnSTS2 126:qnEST1 127:qnEST2 128:qnEST3 129:qnEST4 130:qnEST5 131:qnEST6 103:EST96 104:EST97 105:EST98 106:EST99 107:EST100 98:EST91 99:EST92 100:EST93 101:EST94 102:EST95

US-08-231-565A-26rst Aug 27 09:14

132:enEST7 133:enEST8 134:enEST9 135:enEST10 136:enEST11 137:enEST12

scale 3,102 Mean 12.077; Variance 3.893;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score Match Len	Length DB 1D 621 114 N2	Length DB 1D 621 114 N2	ID 4 N2	1 2	28	Description	. g   g
25.0 621 114 NZ 25.0 621 136 HS 22.8 638 114 NZ	5.0 621 114 N28 5.0 621 136 HS7 2.8 638 114 N28	114 N28 136 HS7 114 N28	4 N28 6 HS7 4 N28	∞ ~ œ	3 00 m	57al2.rl Homo sapi 57al2.rl Homo sapi 57cl2.rl Homo sapi	
496 22.8 638 136 HS7 426 19.6 546 136 HS7	2.8 638 136 HS7 9.6 546 136 HS7	136 HS7 136 HS7	HS7 HS7	ST	36264 46262	67c12.rl Homo s 67f11.rl Homo s	
426 19.6 546 1	9.6 546 114	114	4.	N287	9	rl Homo s	0
420 19.3 430 130 H3	9.3 430 130 HZ	130 H3 113 N2	Z Z	N231	3118		
405 18.6 431 113	8.6 431 113	113	-	N231	3111	в1 Ношо	·
405 18.6 431 129	8.6 431 129	129		HS11	HS111256	sl Homo	0 0
17.5 521 131 HS	7.5 521 131	131		HS29	0283	17	
351 16.2 416 68 R	.2 416 68 R	68 R	~	R7847	_	rl Homo s	0.00e+00
273 12.6 306 83	.6 306 83	83		T2972		mo sap	76e-29
258 11.9 286 46 R01	.9 286 46 R01	46 R01	. R01	R0150	• 5	년 일 :	9.86e-27
54 2.5 58	5 58 113	130		N231	0	yx6/fil.sl Homo saple	
2.0 139 82 T	.0 139 82 T	82 T	E-	T2555	3	Mus musculus	2.58e-17
43 2.0 141 119	.0 141 119	1119		MUSG	MUSGS00442		2.58e-
43 2.0 141 45 MUS	.0 141 45	45		MUSGS	00442	3'-direct	.58e-1
319 66	319 66	99		R7199	4.	j84b09.rl Homo sapi	2.58e-17
43 2.0	.U 336 69 F	110	<u>.</u>	N428	87	yjzogug.ri nomo sapie vv08b05.rl Homo sapie	2.58e-1
41 1.9 151 78 1	.9 151 78 1	78.	_	T0469	. 2	dopsis thali	2.29e-1
41 1.9 153 130 HS	153 130	130		HS16	5282	34f10.rl Homc	2.29e-
42 1.9 207 64 R661	9 207 64 R661	64 R661	R661	R6617	4	rl Homo sapi	2.45e-16
41 1.9 208 8	8 807	œ		H1423		1 Homo sapi	.29e-1
8 42 1.9 219	219 69	69		R8142		Homo sapi	2.45e-16
42 1.9 260 65	260 65	3 5		R6993		1 Homo saple	7.45e-1
31 41 1.9 281 132 H5341.	9 281 132	112		N223	T	į (	2.29e-1
42 1.9 333 5 H	9 333 5 H	7.	-	H0605	. ~	Homo 6	2.45e-16
41 1.9 336 109	9 336 109	109		H926	87	yt90b07.r1 Homc	2.29e-
4 41 1.9 347 1 A	9 347 1			ATTS2	98	chaliana trans	3e-15
5 41 1.9 360 131 HS	9 360 131	131		HS27	1255	sl Homo	2.29e-1
6 41 1.9 360 113 N23	9 360 113 N2	113 N2	N2	N232	71	5.sl Homo sapi	2.29e-
7 42 1.9 391 125	9 391 125	91 125		6159	ο.	STS CHLC.UTK	7.45e-1
8 41 1.9 417 72 R9252	9 417 72 R9252	17 72 R9252	R9252	R9252	6	Homo sapi	7
1 1.9 427 24	427 24	27 24		H6724	2	rl Homo s	2.29e-15
41 1.9 430 59 R492	430 59	30 59		R4927	_	1 Ношо ва	.29e-1
2 1.9 444 130 HS1	444 130 HS1	44 130 HS1	HS1	2	5291	1 Ношо вар	2.45e-
41 1.9 468 8 H14	468 8 H14	68 8 H14	H14	4		1 Homo s	29e-1
40 1.8 295 1.18 N.39	295 118 N3	95 118 N3	18 N3	2 5	04	Cobuz.si Homo sap	Z. U.9e-
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ALIGNMENTS

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	04-JAN-1996 ar to melanocyte		e 2NbHM host=DH10B e. 1st stran	T-3'], o RI adapters	ary from normal r. Anthony P		steichthyes; ; Theria;	2	arra, M.,	r. alid		80	contact the information.			; 9; Gaps 9;
101	simil rsor,		human clone=266782 primer=T7 library=Soares melanocyte 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. 1st str.	CDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGGGCCGCGAGTTTTTTTTT	(Fnarmacia), digested With Not 1 and Eloned into the Not 1 and Eco Ristes of a modified DTT3 vector (Pharmacia). Library CND Structed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P.	,	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Extheria: Archorta: Deimates Catarthin; Hominidae; Homo		Hiller, L., Clark, W., Mundue, I., Eliscon, R., Rakalis, R., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,	, monicularin,		ouis, MO 63108	ugh LLNL ; c r further in		8 others	Length 621 Indels
8107 47000 104-00-00	mRNA EST cDNA clone 266782 5' coprotein gp100 prec		library=Soar n a modified Not I Rsite	oligo(dT) CCCCAGTTTTTT selected, l	. I and clone rector (Pharm nd M.Fatima I was kindly pr		Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata; Deuterostomia, Chordata; Vertebrata; Gnathostomata; Osarcoptesyglis, Chonatata; Tetrapoda; Amniota; Mammalia Eurhosia, Erchonta, Derimatea, Catarbini, Umminidae, Eurhosia, Erchonta, Derimatea, Catarbini, Umminidae,		T., Le,M.,	IIIIamson, A.		Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800	Eax: 314 286 1810 Email: estéwatson.wustl.edu Email: estéwatson.wustl.edu High quality sequence stops: 398 Source: IMAGE Consortium, LIANL This clone is available royalty-free through LIAL; IMAGE Consortium (info@image.llnl.gov) for further:	"sue	145 t	,542; DB 114; No. 0.00e+00; Mismatches 15;
<b>;</b>	p mRNA siens cDNA c 8 glycoprot		primer=T7 ] macia) with	h a Not I - GTGGGAGCGC A was size	ied with Not ied pT/T3 v o Soares ar is (FS374) w		data; Verte mata; Tetra nata; Tetra		M., Kucaba, L., Rohlfir	Scon, K., W	Project	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800	Fax: 314 286 1810 Email: est@wateon.wustl.edu High quality sequence stops: 398 Source: IMAGE Consortium, LINL This clone is available royalty- IMAGE Consortium (info@image.lln	Qualifiers ="Homo sapiens" 56782"	nan" 173 g	Score Pred. 0; N
	621 bp rl Homo sapie 53668 A53668 - human ;.		one=266782 T7T3D (Phar lin resista	primed wit ACCAATCTGAA tranded cDN	la), digest of a modif ted by Bent melanocyte	iens	ae; Metazoa tomia; Chor rygii; Choa rygii; Choa	s 1 to 621)	., Hultman, J., Rifkin,	s, E., Marei	The WashU-Merck EST Project Unpublished (1995)	Contact: Wilson RK WashU-Merck EST Project Washington University S 4444 Forest Park Parkwa Tel: 314 286 1800	Fax: 314 286 1810 Enail: set@watson.wustl.edu High quality sequence stops: Source: IMAGE Consortium, Li This clone is available roy; IMAGE Consortium (info@image	NCBI gi: 1146964 Location/Qualifiers 1621 /organism="Homo sap	/note="numan" <1>621 a 170 c	25.0%; arity 96.2%; Conservative
±			human cl vector=p (ampicil	CDNA was [5'-TGTT] double-s	(Fnarmacia), RI sites of constructed foreskin mel		Eukaryot Deuteros Sarcopte	1 (base	Holman, M Parsons,	Trevaskis Wilson, R.	The Wash Unpublis	Contact: WashU-Me Washingt 4444 For	Fax: 314 Email: e High qua Source: This clo		r 125	Simil 34;
AUS 27 U7.14	LOCUS DEFINITION	ACCESSION NID KEYWORDS	SOURCE			ORGANISM		REFERENCE	AUTHORS		TITLE JOURNAL COMMENT			FEATURES source	mRNA BASE COUNT ORIGIN	Query Match Best Local : Matches 6

CRITARARARARA
1281 AAASTATTACAGGTTCCTGGGCCCCTGGTACATGGTACAGCCACTTAAGGCT 129 agagcagtaccccggattqttctttqtatcqatatgqtccttttcgtcact 131 in

61 aaagtattacaggttccctgggcccctgctggatggtacagccaccttaaggctggtga 120

q

/organism="Homo sapiens" /clone="266782" /note="human"

...>621

mRNA

Location/Qualifiers

information. NCBI qi: 1146964

source

SSEEEEEEES

Key

human

ı

q1146972

US-08-231-565A-26.rst

vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Not\_I Rsite2=Eco RI Male. 1st strand

human clone=266806 primer=T7 library=Soares melanocyte 2NbHM

(Pharmacia), digested with Not I and cloned into the Not I and Eco double-stranded cDNA was size selected, ligated to Eco RI adapters

5'-rettaccaarcreaagregeaeceececagrettrrrrrrrrrrrr-3'),

cDNA was primed with a Not I - oligo(dT) primer

foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal

Homo sapiens

Albino.

121 agagacaagtcccctggattgtgttctgtatcgatatggttccttttccgtcaccctgg 180

04-JAN-1996

yx67c12.r1 Homo sapiens cDNA clone 266806 5' similar to SP:PIR:A53668 A53668 Glycoprotein gp100 precursor, melanocyte

mRNA

638 bp

N28736

DEFINITION

3

RESULT LOCUS

9 1321 CTAGAGAGCTACCTATCCCTGAGCCTGAAGGTCCAGATGCCAGCTCAATCATGTCTACGG 1380 61 aaagtattacaggttccctgggccccctgctggatggtacagccaccttaaggctggtga 120 9 Gaps 1 ctagagagetacetatecetgageetgaaggtecagatgeeageteaateatgtetaegg ; 9 Indels 0; Mismatches 20; g δ g 8 유

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 1 (bases 1 to 638)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Sutheria; Archonta; Primates; Catarrhini; Hominidae; Homo 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Washington University School of Medicine /organism="Homo sapiens" High quality sequence stops: 368 Source: IMAGE Consortium, LLNL Location/Qualifiers Email: est@watson.wustl.edu The WashU-Merck EST Project /clone="266806" WashU-Merck EST Project /note="human" Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 NCBI gi: 1146972 1.,638 Wilson, R. source JOURNAL REFERENCE AUTHORS FEATURES TITLE

241 gatgcatttgagctgactgtgtcctgccaaggcgggctgcccaaggaagcctgcatggag

300

1501 ACATIGICCAGGGTAI-TGAAAGTGCCGAGAICCTGCAGGCTGTGCCGTCCGGTGAGGG 1559

acattgtccaggtnatntgaaagtgccgagatcctgcaggctgtgcgtnccggtgagggg

181

301 atctcatcgccagggtgccagcccctgcccaggggctgtgc-agcctgtgctacccagc

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1680 CCAGCCTGCCAGCTGGTTCTGCACCAGATACTGAAGGGTGGCTCGGGGACATACTGCCTC 1739

360 ccagcctgccagctggtctgcaccagatactgaagggtggctcgggggacatactgcctc

419

479

539

595

359

10 others 153 173 <1..>638 169 133 mRNA BASE COUNT

Length 638; Score 496; DB 114; Pred. No. 0.00e+00; Best Local Similarity 95.5%; Matches 547; Conservative 22.8%; Query Match ORIGIN

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ggtcaagaagcaggccttggnaaggttccgctgatccgtgggcancttgctggtgttgat

480

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1859 GCCTGTGGTCCTTGCATCTCTGATATATAGGCGCAGACTTATGAAGCAAGACTTCTCCGT 1918

ggctgtgggcctttcatctctgntatataggc-ca-acttatgaagcaa-actt-tncgt

540

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1740 AATGTGTCTCTGGCTGATACCAACAGCCTGGCAGTGGTCAGCACCCAGCTTATCATGCCT 1799

420 aatgtgtctctggctgataccaacagcctggcagtggtcagcaaccagcttatcatgcct

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ORGANISM ACCESSION KEYWORDS SOURCE QIN S 6 121 agagacaagtcccctggattgtgttctgtatcgatatggttccttttccgtcaccctgg 180 9 Gaps 1 ctagagagetacctatccetgagectgaaggtccagatgccagetcaatcatgtctacgg ; contact the IMAGE Consortium (info@image.llnl.gov) for further 6 Score 542; DB 136; Length 621; Indels Sequence 621 BP; 125 A; 170 C; 173 G; 145 T; 8 other; US-08-231-565A-26.rst 0; Mismatches 15; Pred. No. 0.00e+00;

25.0%;

Best Local Similarity 96.2%;

Query Match

Conservative

604;

Matches

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1560 GATGCATTTGAGCTGACTGTGTCCTGCCAAGGGGGGCTGCCAAGGAAGCCTGCATGGAG 1619

В ð g ò 음

δ

300

359

1620 ATCTCATCGCCAGGGTGCCAGCCCCTGCCCAGGGGTGTGCCAGCCTGTGCTACCCAGC 1679

360 ccagcctgccagctggttctgcaccagatactgaagggtggctcggggaacatactgcct 419

caatgigiciciggicigataacaaacageciggicagiggicageaceeageitaicaige 479

420

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1857 ATGCCTGTGCTCCTTGCATCTCTGATATAGG 1889

540 atgnetgtgg-cettgnaccettataaaatagg

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US-08-231-565A-26.rst

Length 638; DB 136; Score 496; DB 136; Pred. No. 0.00e+00; 22.8%; 95.5%; Similarity Query Match Local

Gaps 9 Indels 20; Mismatches 547; Conservative Matches

9

1321 CTAGAGAGCTACCTATCCCTGAGCCTGAAGGTCCAGATGCCAGCTCAATCATGTCTACGG 1380 9 1 ctagagagctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacgg 요 δ

120 aaagtattacaggttccctggcccctgctggatggtacagccaccttaaggctggtga 61 셤 8

1441 AGAGACAAGTCCCCCTGGATTGTGTTCTATTCGATATGGTTCCTTTTCCGTCACCCTGG 1500 agagacaagtococctggattgtgttctgtatcgatatggttccttttccgtcaccctgg 180 121 g δ 240 셤 à

300 gatgcatttgagctgactgtgtcctgccaaggcgggctgcccaaggaagcctgcatggag 241 q

1560 GATGCATTTGAGCTGACTGTGCCTGCCAAGGCGGGCTGCCCAAGGAAGCCTGCATGGAG 1619 δ

atctcatcgccagggtgccagcccctgcccagcggctgtgc-agcctgtgctacccagc 359 301 g 8

419 ccagcctgccagctggttctgcaccagatactgaagggtggctcgggggaacatactgcct 360 g

1680 CCAGCCTGCCAGCTGGTTCTGCACCAGATACTGAAGGGTGGCTCGGGGA-CATACTGCCT 1738 ò

caatgtgtctctggctgataacaaacagcctggcagtggtcagcaccagcttatcatgc 479 1739 CAATGTGTCTCTGGCTGATACCAA-CAGCCTGGCAGTGGTCAGCACCCCAGCTTATCATGC 1797 420 염

480 ctgtcaagaacaaggccttggnaaggttccgctgatcgtggggcatcttgctggtgtta ð 염

1798 CIGGICAAGAAGCAGGCCTIGGGCAGGIICCGCTGAICGIGGG-CAICIIGCIGGIGIIG 1856

ð

540 atgnctgtgg-ccttgnacccttataaaatagg 571 = = g

1857 ATGGCTGTGGTCCTTGCATCTCTGATATAGG 1889

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Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;

"The WashU-Merck EST Project";

Unpublished.

yx67c12.r1 Homo sapiens cDNA clone 266806 5' similar to SP:PIR:A53668 A53668 glycoprotein gpl00 precursor, melanocyte

05-JAN-1996 (Rel. 46, Created) 05-JAN-1996 (Rel. 46, Last updated, Version 1)

H

HS736264 standard; RNA; EST; 638 N28736;

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Raplorhini; Catarrhini; Rominidae

Homo sapiens (human) lineage - human ;.

1-638

T 5 HS746262 standard; RNA; EST; 546 BP RESULT

05-JAN-1996 (Rel. 46, Created)
05-JAN-1996 (Rel. 46, Last updated, Version 1)
yx67fll.rl Homo sapiens cDNA clone 266829 5' similar to
SP:PIR:A53668 A53668 Glycoprotein gpl00 precursor, melanocyte lineage - human ;. 

1 - 546

Homo sapiens (human)

est@watson.wustl.edu High quality sequence stops: 368 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further

organism="Homo sapiens"

source

/clone="266806"

Location/Qualifiers

information. NCBI gi: 1146972

Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

Hominidae

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae

Unpublished.

Query Match

셤 ð 셤 à g

**IIRNA** 

source

182

δ 셤 ò g ð 임 à

242

302

362

g δ දු N28746

RESULT LOCUS

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(ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. 1st strand 11; Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, This clone is available royalty-free through LINL; contact the vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B Consortium (info@image.linl.gov) for further information. 62 cagatgccagctcaatcatgtctacggaaagtattacaggttccctgggcccctgctgg 121 1 (bases 1 to 546)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Ie,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Gaps 2 catniacagagigggggagaccacagciagagagciacciatcccigagccigaaggic 61 yx67f11.r1 Homo sapiens cDNA clone 266829 5' similar to SP:PIR:A53668 A53668 Glycoprotein gp100 precursor, melanocyte human clone=266829 primer=T7 library=Soares melanocyte 2NbHM Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Indels 12; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 546; 9 others 0; Mismatches 16; Score 426; DB 114; Pred. No. 0.00e+00; Washington University School of Medicine 120 High quality sequence stops: 377 Source: IMAGE Consortium, LINL

Best RESULT LOCUS g S g გ g g, g S 원 Ç, g 9 g g, g S 1414 ATGGTACAGCCACCTTAAGGCTGGTGAAGAGACAAGTCCCCCTGGATTGTGTTTCTGTATC 1473 1474 GATATGGTTCCTTTTCCGTCACCCTGGACATTGTCCAGGGTAT-TGAAAGTGCCGAGATC 1532 361 GGGCTGCCCAAGGAAGCCTGCATGGAGATCTCATCGCCAGGGTGCCAGCCCCTGCCCAG 165/ 181 gatatggttccttttccgtcaccctggacattgtccaggtnatntgaaagtgccgagatc 241 cggctgtgc-agcctgtgctacccagcccagcctgccagctggttctgcaccaggatact 420 est@watson.wustl.edu High quality sequence stops: 288 Source: IMAGE Consortium, LIAN. This clone is available royalty-free through LIAN. В. atggtacagccaccttaaggctggtgaagagacaagtcccctggattgtgttctgtatc gggctgcccaaggaagcctgcatggagatctcatcgccagggtgccagccctgcccag 29-DEC-1995 (Rel. 46, Created)
29-DEC-1995 (Rel. 46, Last updated, Version 1)
yx67c12.s1 Homo sapiens cDNA clone 266806 3' similar to SP:A41234
A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ;. School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louig, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: 535 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Hilson I "The WashU-Merck EST Project"; Contact: Wilson RK WashU-Merck EST Project Washington University contact the IMAGE Consortium (info@image.llnl.gov) for further Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. ctggcagttggtnaagcaacccactttatcatgnctgggncaagaaacaggnctt BP; 114 A; 107 C; 115 G; 93 T; 1 other; /organism="Homo sapiens" BP. Location/Qualifiers standard; RNA; EST; 430 /clone="266806" information. NCBI gi: 1137268 /note="human" ...>430 (human) Homo sapiens Sequence 430 Unpublished HS118284 N23118; source 1 - 4301593 122 182 362 421 481 mRNA 302 9 à g 8 임 ð 원 δ g ð 쇰 ð 엄 ð 

US-08-231-565A-26 rst Aug 27 09:14

melanocyte Male. double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco yx67c12.s1 Homo sapiens cDNA clone 266806 3' similar to SP:A41234 A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ;. ;; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; foreskin melanocytes (FS374) was kindly provided by Dr. Anthony 2132 CAGGCTCTGAGTATTTATTTCAGTTAATAGTAGTCTCCCCAGGGAAGACTGGGGGAAATAT 2073 2013 1832 CAGCGGAACCTGCCCAAGGCCTGCTTCTTGACCAGGCATGATAAGCTGGGTGCT-GACCA 1774 Sarcopterygli; Choanata; Tetrapoda; Amilota; Mammalla; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 430)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 120 240 300 360 9 Gaps Rolman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. aggtgtttctgtcaactccaggaaaatcacagcatcatatgagagtactcagacctgctg cagecaqtgactgctgctatqtggcaactggggtacggagaagtcttgcttcataagtct gegectatatateagagatgeaaggaceacagecateaaeacageaagatgeceaegat cageggaacetgeceaaggeetgettettgaceaggeatgataagetgggtgettgaeea RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 1 caggototogagtatttatttcagttaatagtagtotoccagggaagactgggggaaatat human clone=266806 primer=m13 -40 forward library=Soares 1; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Indels Length 5; DB 130; Pred. No. 0.00e+00 0; Mismatches Score 420; 19.3%; 96.38; Conservative 1713 TCAGTATCTG 1704 Homo sapiens 421 tcaqtatctq 430 Similarity g1137268 Albino. 427; Query Match Local œ DEFINITION ORGANISM Matches 61 181 241 301 ACCESSION KEYWORDS SOURCE REFERENCE AUTHORS

JOURNAL

TITLE COMMENT

US-08-231-565A-26rst

source

FEATURES

BASE COUNT ORIGIN

IIRNA

Matches

셤 g 염 გ 1773

გ 용

1832 361

g, g

301

8

1952

g

g გ 용

a

1892

გ

241

1713

421

US-08-231-565A-26.rst Aug 27 09:14

human clone=266782 primer=m13 -40 forward library=Soares melanocyte double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. yx67a12.s1 Homo sapiens cDNA clone 266782 3' similar to SP:A41234 A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; ŝ This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 2132 CAGGCTCTGAGTATTTATTTCAGTTAATAGTAGTCTCCCAGGGAAGACTGGGGGAAATAT 2073 61 aggtgtttctgtcaactccaggaaaatcacagcatcatatgagagtactcagacctgctg 120 1 caggctctgagtatttatttcagttaatagtagtccccagggaagactgggggaaatat 60 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Huchan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 28-DEC-1995 Gaps Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo 1444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 .. .. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 431; 1 others Indels Score 405; DB 113; Pred. No. 0.00e+00; Washington University School of Medicine 0; Mismatches ų 8 /organism="Homo sapiens" /clone="266782" High quality sequence stops: 286 셤

US-08-231-565A-26.rst

(ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. 1st strand yx80c07.rl Homo sapiens cDNA clone 268044 5' similar to PIR:A53668 RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Deuterostomia, Chordata, Vertebrata; Gnathostomata, Osteichthyes; Sarcopterygii, Choanata; Tetrapoda, Amniota; Mammalia, Theria, ÷, A53668 glycoprotein gp100 precursor, melanocyte lineage - human vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B 1892 GCGCCTATATATCAGAGATGCAAGGACCACAGCCATCAACACCAGCAAGATGCCCACGAT 1833 2012 CCCACTGAGGAGGGGGCTGTTCTCACCAATGGGACAAGAGCAGAAGATGCGGGGTAGACG 1953 cccactgaggagggtattttcaccaatgggacaagagcagaagatgcggggtagacg 180 240 300 360 420 61 aggtgtttctgtcaactccaggaaaatcacagcatcatatgagagtactcagacctgctg 120 S 22-JAN-1996 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Gaps human clone=268044 primer=T7 library=Soares melanocyte 2NbHM cttgccaggctgttggtatcagccagagacacatttgaggcagtatgtncccgagccacc 181 cagccagtgactgctgctatgtggcaactggggtacggagaagtcttgcttcataagtct 241 gegectatatateagagatgeaaggaceacagecateaacaceageagatgeceacgat 301 cageggaacctgeccaaggecttgettettgaccaggeatgataagetgggtgetgacca 1 caqqctctqaqtatttatttcaqttaataqtaqtctcccaqqqaaqactgqqqqaaatat Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo ÷ Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Indels cDNA was primed with a Not I - oligo (dT) primer Pred. No. 0.00e+00; 0; Mismatches mRNA. 521 bp 98.88; (bases 1 to 521) Conservative 1715 CTTCAGTAT 1707 Best Local Similarity 421 cttcagtat 429 q1163835 N40290 Albino. N40290 424; Ξ DEFINITION 121 361 ORGANISM Matches ACCESSION REFERENCE AUTHORS KEYWORDS RESULT g g 쇰 ც 염 c<sub>D</sub> 음 გ 쇰 g, g გ 임 g 셤 g

AGGIGITICIGICAACICCAGGAAAATCACAGCAICAIATGAGAGIACICAGACCIGCIG 2013 2012 CCCACTGAGGAGGGGGCTGTTCTCACCAATGGGACAAGAGCAGAAGATGCGGGGTAGACG 1953 CAGCGGAACCTGCCCAAGGCCT-GCTTCTTGACCAGGCATGATAAGCTGGGTGCTGACCA 1774 cocactgaggaggggtattctcaccaatgggacaagagcagaagatgcggggtagacg 180 cagcggaacctgcccaaggccttgcttcttgaccaggcatgataagctgggtgctgacca 360 181 cagccagtgactgctgctatgtggcaactggggtacggagaagtcttgcttcataagtct 240 gcgcctatatatcagagatgcaaggaccacagccatcaacaccagcaagatgcccacgat 300 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., est@watson.wustl.edu High quality sequence stops: 286 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL 29-DEC-1995 (Rel. 46, Created)
29-DEC-1995 (Rel. 46, Last updated, Version 1)
yx67a12.s1 Homo sapiens cDNA clone 266782 3' similar to SP:A41234
A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ; School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: the IMAGE Consortium (info@image.llnl.gov) for further Contact: Wilson RK WashU-Merck EST Project Washington University Vertebrata; Mammalia; Catarrhini; Hominidae. BP; 114 A; 105 C; 116 G; 95 T; 1 other; /organism="Homo sapiens" Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini; В. Location/Qualifiers HS111256 standard; RNA; EST; 431 /clone="266782" "The WashU-Merck EST Project"; /note="human" information. NCBI gi: 1137261 <1..>431 1..431 Homo sapiens (human) 1715 CTTCAGTAT 1707 cttcagtat 429 Sequence 431 Unpublished contact Aug 27 09:14 N23111; source 1 - 4312072 1892 1832 1773 121 241 301 421 361 EST. გ g 요 S 염 გ გ 임 g 용 염 გ 음

DB 129; Length 431;

Score 405;

18.6%;

Query Match

US-08-231-565A-26.rst

Aug 27 09:14

yx80c07.r1 Homo sapiens cDNA clone 268044 5' similar to PIR:A53668 A53668 glycoprotein gp100 precursor, melanocyte lineage - human ;.

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

est@watson.wustl.edu High quality sequence stops: 340 Source: IWAGE Consortium, LINE This clone is available royalty-free through LINE; contact the IWAGE Consortium (info@image.llnl.gov) for further

Gaps 4; 521; 1; Indels Score 380; DB 131; Length Pred. No. 0.00e+00; 0; Mismatches

4;

9 1 atgaccetagtggetatetggetgaagetgaceteteetacacetgggaetttggagaca 61 gtagtggaaccetgatetetegggcaettgtggtcaetcataettaeetggageetggee 120 

121 cagtcactgcccaggtggtcctgcaggctgccattcctctcacctcctgtggctcctccc 180

181 cagttccaggcaccacagatgggcacaggccaactgcagaggccctaacaccacagctg 240 

361 agaatgcccaactgcagagagcacaggtatggacacctggagaaggtgcc 410

1132 AGA-TGCC-AACTGCAGAGAGCACCACAGGTATG-ACACCTG-AGAAGGTGCC 1177

Aug 27 09:14

Based Upon 52 Million Basepairs of cDNA Sequence Tel: 3018699056 Fax: 3018699423 q611824 T29726 T29726 RESULT 14 ORGANISM 301 361 ACCESSION JOURNAL REFERENCE AUTHORS KEYWORDS COMMENT SOURCE g ð 음 δ 염 ð g ò 유 (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsitel=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 9 yi73d06.rl Homo sapiens cDNA clone 144875 3' similar to SP:A41234 A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ; Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. , This clone is available royalty-free through LINL; contact the 1327 AGCTACCTATCCCTGAGCCTGAAGGTCCAGATGCCAGCTCAATCATGTCTACGGAAAGTA 1386 IMAGE Consortium (info@image.llnl.gov) for further information. human clone=144875 library=Soares placenta Nb2HP vector=pT7T3D 61 ttacaggttccctgggcccctgctggatggtacagccaccttaaggctggtgaagagac 120 1 agctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacggaaagta 60 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Gaps 09-JUN-1995 1 (bases 1 to 416) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 0; Mismatches 13; Indels 6; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found. Length 416; 3 others Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine Query Match 16.2%; Score 351; DB 68; Best Local Similarity 95.4%; Pred. No. 0.00e+00; 103 t /organism="Homo sapiens" High quality sequence stops: 320 Source: IMAGE Consortium, LLNL 119 g **IIRNA** Location/Qualifiers Email: est@watson.wustl.edu The WashU-Merck EST Project /clone="144875" /note="human" 416 bp 113 c 397; Conservative Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 NCBI gi: 854770 1..416Homo sapiens æ Wilson, R. 78 g854770 R78477 source Matches DEFINITION BASE COUNT ORGANISM TITLE JOURNAL ACCESSION NID KEYWORDS SOURCE REFERENCE AUTHORS FEATURES ORIGIN

181 giccagginatitgaaagigccgagatccigcaggcigigcgitccggigagggggaigc 240

241 atttgagctgactgtgtcctgccaaggcgggctgcccaaggaagcctgcatgggagatct 300

catogocagggtgccagcccctgcccagcngctgtgccagcctgtgcttacccagccca 360

1624 CATCGCCAGGGTGCCAGCCCCTGCCCAGGGGTTGTGCCAGCCTGTGCT-ACCCAGCCCA 1682

gccttgncagttggtttttgcaccagatacttaagggttggttggggacatattgc 416

DEFINITION EST92123 Homo sapiens cDNA 5' end similar to melanocyte-specific protein Pmel 17 (GB:M77348) (HT:1391). mRNA 306 bp

human primer=M13 Reverse library=Human Skin. Homo sapiens

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., ! (bases 1 to 306)

Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Handlom, E., Hinkle Jr. P.S., Kelley, J.M., Klimck, K.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,

Pellegrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dinke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G. A., He, W. -W., Hu, J. -S., Greene, J. M., Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Ji, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y. -F., Wing, J., Xu, C., Yu, G. L., Kuben, S. M., Dillon, P. J., Fannon, M. R., Rosen, C. A., P. V., C. J., R. Weissner, P. S., Olsen, W., Dillon, P. J., Fannon, M. R., Rosen, C. A., P. V., C. J., R. Weissner, P. S., Olsen, C. A., Fannon, M. R., Rosen, C. A., C. J., R. Weissner, P. S., Olsen, C. A., Fannon, M. R., Rosen, C. A., Fannon, M. R., Fannon, M. R., Fannon, M. R., Fannon, G. A., Fannon, G. F Initial Assessment of Human Gene Diversity and Expression Patterns Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C

The Institute for Genomic Research Other ESTs: THC20616 Contact: Venter, JC Unpublished (1995

932 Clopper Rd, Gaithersburg, MD 20878

for clone availability, additional sequence and expression Smail: tdbinfo@tdb.tigr.org

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Unpublished (1995)

JOURNAL

US-08-231-565A-26 rst

COMMENT ð ð STRANG CDNA was primed with a Pac I - oligo (dT) primer [5' AACTGGAAGAATTAATTAAACATCTTTTTTTTTTTTTT 3'], double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 R01509 286 bp mRNA EST 31-MAR-1995 ye79a02.r1 Homo sapiens cDNA clone 123914 5' similar to SP:A41234 A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ;. ; information related to this EST, please contact the TIGR Database human clone=123914 library=Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st 1324 GAGAGCTACCTATCCCTGAGCCTGAAGGTCCAGATGCCAGCTCAATCATGTCTACGGAAA 1383 1444 GACAAGTCCCCCTGGATTGTGTTCTGTATCGATATGGTTCCTTTTCCGTCACCTGGACA 1503 121 gacastccccctgsttgtnttctgtatcgatatggttcttttccgtnaccctggaca 180 61 gtattacaggttccctgggcccctgctggatggtacagccaccttaaggctggtgaaga 120 1 gngagctacctatccctgagcctgaaggtccanatgccagctcaatcatgtctacggaaa 60 Gaps 1564 CATTICAGCT-CACTGTGTCTCCCCAAGGCGGCTGCCCAAGGAA-GCCTGCATGC 1617 24] catttgagcttgactgtgtcctgccaaggogggctgccaaggaaagcctgcatgg 296 5; Length 306; 5 others Indels Score 273; DB 83; Pred. No. 4.76e-298; 0; Mismatches 75 /organism="Homo sapiens" Location/Qualifiers 86 g /note="human" (tdbinfo@tdb.tigr.org) 12.6%; 97.0%; 77 c 287; Conservative <1..>306 1..306 NCBI gi: 611824 Best Local Similarity æ 63 q751245 R01509 EST. Query Match 15 DEFINITION source SASE COUNT mRNA Matches ACCESSION KEYWORDS SOURCE FEATURES ORIGIN

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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Possible reversed clone: similarity on wrong strand Washington University School of Medicine Trace considered overall poor quality High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LINI WashU-Merck EST Project Contact: Wilson RK

ö Length 286; 4 others Score 258; DB 46; I Pred. No. 9.86e-279; 29 /organism="Homo sapiens" 87 g Location/Qualifiers /clone="123914" /note="human" / Match 11.9%; Local Similarity 94.7%; 2 98 1..286 æ 20 Query Match source BASE COUNT Matches FEATURES ORIGIN

NCBI gi: 751245

ö Gaps 0; Mismatches 15; Indels 269; Conservative

1487 ITCCGTCACCCTGGACATTGTCCAGGGTATTGAAAGTGCCGAGATCCTGCAGGCTGTGCC 1546 1 ttccgtcaccctggacattgtcngggaatttgaaagtgccgagatcctgcaggctgtgcc 60 염 ð

61 incccgigaggggatgcatttgagctgactgtqtcctgccaangcgggctgcccaagga 120 염 ò a

ð 셤

1727 GACATACTGCCTCAATGTGTCTCTGGCTGATACCAACAGCCTGG 1770 241 gacatactgcctcaatgtgtctctggctgataccaacagcctgg 284 염

Search completed: Tue Aug 27 09:27:25 1996 Job time : 865 secs.

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 286)

REFERENCE AUTHORS

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

The WashU-Merck EST Project

TITLE

Wilson, R.

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

vector. Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo

Homo sapiens

ORGANISM

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Aug 27 08:12:54 1996; MasPar time 13.38 Seconds 436.417 Million cell updates/sec Run on:

not generated. Tabular output

>US-08-231-565A-27 Title:

1 MDLVLKRCLLHLAVIGALLA.....RIFCSCPIGENSPLLSGQQV 661 (1-661) from US08231565A.pep 4698 Description: Perfect Score: Sequence:

**PAM** 150 Gap 11 Scoring table:

76839 seqs, 8833555 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq23 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15

Mean 36.948; Variance 191.419; scale 0.193 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	ult No. Score		% Query Match Length DB ID	DB	01	Description	Pred. No
	1 4698	ļ		13	R84854	MART-1 melanoma antiq	0,00e+00
	2 4684			661 14	R78646	Melanoma associated a 0.00e+00	0.00e+00
	3 4679			15	-	MART-1 melanoma antiq	0.00e+00
	4 238			9	R30054	Melanoma cell surface	
	5 206			-	P91941	Sequence of preprospa	
	6 172			7	R07670	Intestinal mucin dedu	8.21e-0
	7 176	3.7	278 2	7	R07671	Intestinal mucin dedu	4.35e-04
	8 174			ო	R12535	SMUC-41 intestinal mu	5.98e-04
	9 169			14	R80144	EBV qp350/220.	
1	0 169			m	P50073	Epstein-Barr virus (E	
-	1 165			m		SMUC-40 intestinal mu	
-	2 162			Ξ		Host cell factor prot	3.97e-03
						•	

8.66e-03	3.48e - 02	4.05e-02	4.05e-02	4.05e-02	4.05e-02	4.05e-02	6.40e - 02	4.05e-02	1.17e-01	1.17e-01	8.68e-02	1.01e-01	7.46e - 02	2.14e-01	2.14e-01	3.90e-01	4.52e-01	8.17e-01	8.17e-01	8.17e-01	9.46e - 01	8.17e-01	1.96e+00	1.27e+00	1.27e+00	2.27e+00	2.62e+00	2.62e+00	4	3.49e+00	3.02e+00	4.65e+00
Polyhydroxyalkanoate	Streptococcus faecali	Bile salt-activated 1		Human milk bile-salt	BSSL/CEL.	Bile salt-stimulated	Bile-salt stimulated	MSF precursor.	SMUC-53 intestinal mu	Intestinal mucin dedu	P. communis (pear) ar		Yeast 4.7 kB agglutin	Bile salt-stimulated	Bile salt-stimulated	Eimeria cell surface	Unique sequence fragm	SMUC-87 intestinal mu	Intestinal mucin dedu	Cotton fiber-specific	Soluble CD43 fragment	CREB binding protein.	Merozite surface anti		Sequence of extracell	Filamentous haemagglu	P-selectin ligand.	hsp150.	PS1 protein from C.me	Sequence of the Falci	Serum opacity factor	Transmembrane form of
R53915	R85290	R75107	R58984	R14311	R45189	R58980	R20098	R26049	R12537	R07673	R75511	R48993	R60562	R70145	R58983	P91655	R08034	R12538	R07674	R86913	R14552	R79054	R05879	R67652	P60723	R05041	R85076	R41547	R32657	P60570	R70126	R23973
252 10	671 15	722 14	722 11	742 3	744 8	745-11		1404 5		132 2	1	1026 9	1537 11		668 11	259 1	486 2	119 3		214 15	235 3	2441 14			918 3	3647 1	412 15	413 8	657 6	844 3	1025 13	455 4
3.3	3.5	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0	3.0	3.0	5.9	5.9	2.8	5.8	2.7	2.7	2.7	2.7	2.7	5.6	5.6	5.6	5.6	5.2	2.5	2.5	2.5	2.5	2.4
157	148	147	147	147	147	147	144	147	140	140	142	141	143	136	136	132	131	127	127	127	126	127	121	124	124	120	119	119	116	117	118	115
13	14	15	16	17	18	19	20	21	22	23	24	25	56	2.7	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALI GNMENTS

SUL						_	tumour-associated antigen; immunogen; diagnosis; prognosis;	prophylaxis; therapy; vaccine.	Mammalian sp.	I Key Location/Qualifiers			/note= "see R84199"	I W09529193-A2.	02-NOV-1995.						1 WPI; 95-382963/49.			vectors, host cells and antibodies, used to detect, treat and	immunise animal against melanoma.	
2	Ä	Į	υŢ	띰	Ž	₹	Ž	₹	S	E	드	ᇤ	G	N.	PD	PF	Ę.	PR	PA	ΡI	H	DR.	PT	ΡŢ	P	

Claim CDNA2 T-Lym specification of incompared preversion of the control of the	RESULT ID R7	DT 22		KW Me						PR 16			 DR WP		P. 19				රුර		CC ra	-	Query	Best	Match	ż	αn	δ	 qa	ð	?	0b 1	L	, (X	Db 1	0y 1	Db 2	Qy 2	ob 3	٠ م		Db 3	0y 3	Db 4
	T-lymphocytes, and is a derivative of		_	prevention (by immunisation) of melanoma. Antibodies against	and its immunogenic peptides may be used in the detection and	isolation of the antigen from a sample, the detection of which	indicative of a disease state (melanoma or metastatic melanoma)	_	•	Score 4698; DB 15;	Pred. No. 0.00e+00;	0: Mismatches 0: Indels 0: Gaps	1 mdlvlkrcllhlavigallavgatkvprnqdwlgvsrqlrtkawnrqlypewteagrldc	1 MDLVIKRCLLHLAVIGALLAVGAIKVPRNQDWLGVSRQLRIKAWNRQLYPEWIEAQRLDC	[2] separated provides to a separate to be a separate to be a separate to be a separate.		61 WRGGOVSIKVSNDGPTI.GANASPSTAINFPGSOKVI.PDGOVIWVNTIINGSOVAGGOP	121 vypqetddacifpdggpcpsgswsqkrsfvyvwktwgqywqflggpvsglsigtgramlg		121 VYPQETDDACIFPDGGPCPSGSWSQKRSFVYVWKTWGQYWQFLGGPVSGLSIGTGRAMLG	) 1   mm   1   1   mm   1 mm   1 mm   1   1	TOT CHICKENCY VILLEGE BY VETERIBES BEALCICULOUS PROPERTIES THE CONTRACT OF THE	181 THIMEVIVYHRRGSRSYVPLAHSSSAFIIIDQVPFSVSVSQLRALDGGNKHFLRNQPLIF		241 alqlhdpsgylaeadlsytwdfgdssgtlisralvvthtylepgpvtagvvlqaaiplts		241 ALQLHDPSGYLAEADLSYTWDFGDSSGYLISKALVVTHTYLEFGFVTAQVVLQAAIPLTS	301 cgsspvpgttdghrptaeapnttaggvpttevvgttpggaptaepsgttsvgvpttevis	301 CGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPTAEPSGTTSVQVPTTEVIS	361 tapyomptaestomtoekvpvsevmottlaemstpeatomtpaevsjvvlsottaaovtt		361 TAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTT	101 tammattanalninanandassimatasituslumlidutatlulum	7.	421 TEMVETTARELPIPEPEGPDASSIMSTESITGSLGPLLDGTATLRLVKRQVPLDCVLYRY	481 gsfsvtldivggiesaeilgavpsgegdafeltvscggglpkeacmeisspgcgppagrl	481 GSFSVTLDIVQGIESAEILQAVPSGEGDAFELTVSCQGGLPKEACMEISSPGCQPPAQRL	541 cqpvlpspacqlvlhqilkgqsqtyclnvsladtnslavvstqlimpgqeaglqqvpliv	541 CQPVLPSPACQLVLHQILKGGSGTYCLNVSLADTNSLAVVSTQLIMPGQEAGLGQVPLIV	601 at live mount on live velatormal who only a lave for anni annum linama	out gittvimavviasiijitrimkaatskyaiphessen*iittpiricscpiganspirsgad.	601 GILLVLMAVVLASLIYRRRLMKQDFSVPQLPHSSSHWLRLPRIFCSCPIGENSPILSGQQ	661 v	0v 661 V 661

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9 9	80	09	120 120	180 180	240 240	300	360	420	480
R78646 standard; Protein; 661 AA. R78646; 22-JAN-1996 (first entry) Melanoma associated antigen gp100. Melanoma; antigen; vaccine; immunogen; primer; probe; detection; identification; tumour; gp100. Homo sapiens. EP-668350-A1. 23-AUG-1995, 14-FEB-1995, 200348. 14-FEB-1994, EP-20337. 21-DEC-1994, EP-20337. 21-DEC-1994, EP-203709. ALKO DAKO NOBEL NV. Adema GJ, Figdor GG; WPI: 95-284790/38. N-PSDB; Q96055. Melanoma associated antigen gp100 - used in vaccines and for the detection of tumours Claim 1; Page 22-24; 40pp; English. Immunogenic peptides derived from the melanoma associated antigen may be used in the production of vaccines. Nucleotide sequences encoding the immunogenic peptides may be used as primers and probes in the detection of melanoma cells. Tumour infiltrating lymphocytes capable of binding to the melanoma associated antigen can be	radiolabelled, they may be used to identify tumour deposits. Sequence 661 AA; Query Match Match Matches 660; Conservative 0; Mismatches 1; Indels 0; Gaps	igallavgatkvprngdwlgvsrglrtkawnrglypewteagrldc 	61 wrggqvslkvsndgptliganasfsialnfpgsqkvlpdgqviwvnntiingsqvwggqp 	1. vypqetddacifpdggpcpsgswsqkrsfvyvwktwggywqvlggpvsglsigtgramlg 			cgsspvpgttdghrptaeapnttagqvpttevvgttpggaptaepsgttsvqvpttevis 	tapvqmptaestgmtpekvpvsevmgttlaemstpeatgmtpaevsivvlsgttaaqvtt 	tewvettarelpipepegpdassimstesitgslgplldgtatlrlvkrqvpldcvlyry
R7864 R7864 R7864 R7864 R61an Melan Melan H0m EP-66 23-AU 14-FE 11-FE 21-DE (ALWU Adema MPI; M-PSD Melan Immun min th	rad Seq Seq lery		9 9	121	181	241	301	361	421
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# US-08-231-565A-27.rag $A_{ m ug}~27~08:01$

of the antigen from a sample, the detection of which is indicative of a disease state (melanoma or metastatic melanoma) 661 AA;

Gaps ö 661; 2; Indels Length DB 15; Score 4679; DB 15; Pred. No. 0.00e+00; 0; Mismatches 99.6**8**; 99.7**8**; 659; Conservative Similarity

ö

9 9 1 MDLVIKRCLLHLAVIGALLAVGATKVPRNQDWLGVSRQLRTKAWNRQLYPEWTEAQRLDC mdlvlkrcllhlavigallavgatkvprnqdwlgvsrqlrtkawnrqlypewteagrldc 

120 61 WRGGQVSLKVSNDGPTLIGANASFSIALNFPGSQKVLPDGQVIWVNNTIINGSQVWGGQP 120 wrggqvslkvsndgptliganasfsialnfpgsqkvlpdgqviwvnntiingsqvwggqp 

121 vypqetddacifpdggpcpsgswsqkrsfvyvwktwgqywqvlggpvsglsigvgramlg 180

240 thtmevtvyhrrgsrsyvplahsssaftitdqvpfsvsvsqlraldggnkhflrnqpltf

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RESULT

300 300 

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360

420 420 tapvgmptaestgmtpekvpvsevmgttlaemstpeatgmtpaevsivvlsgttaagvtt TAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTT 

480 tewvettarelpipepegpdassimstesitgslgplldgtatlrlvkrqvpldcvlyry 

480 540

gsfsvtldivqgiesaeilqavpsgegdafeltvscqgglpkeacmeisspgcqppaqrl

9 009 cqpvlpspacqlvlhqilkggsgtyclnvsladtnslavvstqlimpgqeaglgqvpliv 

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661 v 661

R30054 standard; peptide; 30 AA.

05-MAY-1993 (first entry)

Melanoma cell surface protein N-terminal sequence. N-terminal; membrane; bound; ME20; antigen; human; melanoma; tumour;

antibody; immune response

Misc difference

W09221767-A.

Homo sapiens.

181 v-pttpetttvpttpetttvpt-tpetttvpttpetttvpttpetttvp-ttpetttast 237 ation patterns or glycosyltransferase activity. They can be used for the early detection and differential diagnosis of cancers especitivelial cancer, and also in diseases with altered intestinal mucin prodn. such as cystic fibrosis and colitis.

See also R07671-76. glycosyl transferase; familial polyposis coli; Intestinal mucin deduced from clone SMUC 40. Location/Qualifiers Disclosure; Fig 4A; 45pp; English. R07670 standard; protein; 166 AA. 01-NOV-1990. 25-JUL-1989; U03206. 14-APR-1989; US-338710. (REGC) University of California. /label= N-glycosylation site 22-FEB-1991 (first entry) 118..140 141..163 149..151 glycosylation patterns. 95..117 26..48 49..71 72..94 3..25 WPI; 90-348495/46. N-PSDB; Q06483. 'label= repeat 6 /label= repeat 7 /label= repeat 1 'label= repeat 2 /label= repeat 3 label= repeat 5 /label= repeat 4 Modified-site Kim YS; Gum JR Homo sapiens. WO9012892-A R07670: Region Region Region Region Region Region Region RESULT 염 유 ð δ à ö ; comprising residues 21-400, 21-69, 351-400 and 72-348 may also be produced. One or more of residues 1,4,5,8,9,11,20,21,22,24,25,26,33,35, position in one of the other fragments, and/or contg. the exchange D-E, Polypeptide preprospasmolysin and its fragments - derived from Xenopus The peptide has spasmolytic and neurotransmitter functions. Fragments 36 and 42-9 may be replaced by another amino acid present in the same This sequence represent the N-terminal of three major membrane bound ME20 antigens. These antigens have molecular weights 116, 100 and 80 kD respectively and they all have identical N-terminal sequences. These antigens may be recognised by an antibody and the antibody may then be used to determine the presence and locate human melanoma Gaps 7; Gaps administered with a therapeutic agent. This peptide may be used to These antigens are only expressed by human melanoma tumour cells. (PLAC) Max-Plank Ges. Wissensch. Weickmann H, Fincke K, Weickmann F, Huber B, Liska H, Prechtel J, New monoclonal antibody ME20 - specific for cell surface protein detectable on human melanoma tumour cells, for diagnosis and ; 0 The antibody may also be used to treat melanoma when Query Match 4.4%; Score 206; DB 1; Length 400; Best Local Similarity 30.1%; Pred. No. 3.39e-06; induce an immune response directed towards human melanoma 34; Mismatches 80; Indels 5.1%; Score 238; DB 6; Length 30; 10.0%; Pred. No. 1.67e-08; 0; Indels laevis, with spasmolytic and neurotransmitter activities. 0; Mismatches Hellstrom I, Hellstrom KE, Marquardt H; 1 kvprnqdwlgvsrqlrtkawnrqlypewt 29 25 KVPRNQDWLGVSRQLRTKAWNRQLYPEWT 53 Location/Qualifiers Disclosure; Page 20; 38pp; English. /note= "Amino acid not identified" Preprospasmolysin; Xenopus laevis. P91941 standard; peptide; 400 AA. (BRIM ) BRISTOL-MYERS SQUIBB CO. Sequence of preprospasmolysin. Claim 1; page 5; 8pp; german. Best Local Similarity 100.0%; 07-FEB-1990 (first entry) 29; Conservative 52; Conservative I-L, K-R, N-Q and/or S-T. Sequence 400 AA; 28-SEP-1989. 14-MAR-1988; 808456. 14-MAR-1988; DE-808456. 05-JUN-1991; US-710613. treatment of melanoma 10-DEC-1992. 27-MAY-1992; U04451.

WPI; 89-286097/40.

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N-PSDB; N91235

Sequence

Matches

Xenopus laevis

P91941:

RESULT

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122 pdtttasttaetttvpttpetttvpttpetttvpttpetttvpttpetttvpttp-ettt 180 283 PGPVTAQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPT 342 용

343 AEPSGTTSVQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEAT-GMT 401

238 taetttvpttpettteptttpttdttpptlp-ptpetttetttetttet 289

WPI; 92-433665/52

30 AA;

Sequence

cells.

Query Match

Matches .

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using antibody probes. The DNA sequence allows determination of the biochemically because the protein backbone is so heavily glycosylated and conditions required to remove the carbohydrate tend to The sequence was deduced from a clone isolated from a cDNA library Human intestinal mucin DNA, polypeptides and antibodies - used in result in breakage of the protein. Prods, of the DNA can be used to produce Abs useful for detecting hIM and determining glycosyldiagnosis and treatment of e.g. cancers, cystic fibrosis and primary amino acid structure, difficult to characterise Epithelial cancer; cystic fibrosis; ulcerative colitis;

166 AA;

Sequence

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See also R07670-76,

prods. are also useful as substrates for assay of glycosyltransferase A vaccination for inducing a cellular immune response can be prepd. activity and other glycosylation enzymes. See also Q12217-21 and Q12247-51. Sequence Region Region Region Matches g 쇰 g ð ð à 5 gtqtptttpitttttvtptptptgtqtptrtpittttvtptptptgtqtp-tptpittt 126 265 SSGTLISRALVVTHT-YLEPGPVTAQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTT 323 324 AGQVPTTEVVGTTPGQAPTAEPSGT-TSVQVPTTEVISTAPVQMPTAESTGMTPEKVPVS 382 9 stttmvtptptptgtqtltptpittttv-tptptptgtqtptstpisttttvtptptpt 67 Gaps using antibody probes. The DNA sequence allows determination of the primary amino acid structure, difficult to characterise The sequence was deduced from a clone isolated from a cDNA library biochemically because the protein backbone is so heavily glycosylfor the early detection and differential diagnosis of cancers esp. epithelial cancer, and also in diseases with altered intestinal Human intestinal mucin DNA, polypeptides and antibodies - used in diagnosis and treatment of e.g. cancers, cystic fibrosis and result in breakage of the protein. Prods. of the DNA can be used to produce Abs useful for detecting hIM and determining glycosylation patterns or glycosyltransferase activity. They can be used ated and conditions required to remove the carbohydrate tend to 5 Score 172; DB 2; Length 166; Pred. No. 8.21e-04; 37; Mismatches 77; Indels Epithelial cancer; cystic fibrosis; ulcerative colitis; mucin prodn. such as cystic fibrosis and colitis. 127 ttvtptptptgtqtpts-tpittnttvtptptptgtpst 164 383 EVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTTT 421 glycosyl transferase; familial polyposis coli; Intestinal mucin deduced from clone SMUC 41. \_ :: Location/Qualifiers Disclosure; Fig 4B; 45pp; English. R07671 standard; protein; 278 AA. (REGC) University of California. /label= N-glycosylation site Query Match 3.7%; Best Local Similarity 25.2%; 40; Conservative 22-FEB-1991 (first entry) 265..267 99..121 glycosylation patterns. 29..52 53..75 76..98 25-JUL-1989; U03206. 14-APR-1989; US-338710. 6..28 Kim YS, Gum JR WPI; 90-348495/46. N-PSDB; Q06484. /label= repeat 2 'label= repeat 4 /label= repeat 5 /label= repeat 1 /label= repeat 3 Modified-site Homo sapiens. WO9012892-A. 01-NOV-1990. R07671; colitis. Region Region Region Region Region Matches 89

304 SPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPTAEPSGTTSVQVPTTEVISTAP 363 63 tmtptptptstksttvt-pittttvtatptptgt-qtptmipisttttvtptptpttgs 120 ||::|::|::|| 364 VQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEM 423 Gaps 8 Score 176; DB 2; Length 278; Pred. No. 4.35e-04; 41; Mismatches 69; Indels Query Match 3.7%; Best Local Similarity 28.0%; 46; Conservative 278 AA; Sequence

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121 tgppthtstapiaelttsnpppesstpqtsrstsspltesttll 164 | : ||:| :::: || :: || 424 VET-T-ARELPIPEPEGPDASSIMST-ESITGSLGPLLDGTATL 464

SMUC; intestinal mucin; diagnosis; cancer. Location/Qualifiers ż R12535 standard; Protein; 278 R12535; 02-SEP-1991 (first entry) SMUC-41 intestinal mucin. (egion /label= repeat\_1 30..52 .egion /label= repeat\_2 `'-'- 53..75 7..29 label= repeat\_3 Homo sapiens. Cross-links

05-DEC-1989; US-447140. (REGC ) UNIV OF CALIFORNIA. /label= glycosylation\_site W09108217-A. /label= repeat\_5 Modified -site 265..267 99..121 76..98 Kim YS, Gum JR; WPI; 91-193147/26. N-PSDB; Q12218. 04-DEC-1990; U07087. label= repeat\_4 13-JUN-1991.

partic. by blocking or inveriously some resonance phenotype. Intestinal mucin protein which contributes to the neoplastic phenotype. cancer therapy by coupling to toxins and can also be used in treatment, The sequence contains repeats having a threonine and proline-rich partic. by blocking or interrupting some functional activity of Nucleic acid encoding human intestinal mucin peptide(s) - used Antibodies produced against this mucin peptide can be used for for producing prods, for diagnosis and treatment of disorders such as cancer Disclosure; Fig 2(B); 57pp; English. consensus.

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음 9 ë 304 SPVPGTIDGHRPTAEAPNTTAGQVPTTEVVGTIPGQAPTAEPSGTISVQVPTTEVISTAP 363 63 tmtptptptstksttvt-pitttttvtatrtptgt-qtptmipisttttvtptptpttgs 120 364 VOMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEW 423 262 FGDSSGTLISRALVVTHTYLEPGPVTA-QVVLQAAIPLTSCGSS-PVPGTTDGHRPTAEA 319 481 ttsgaspvtpsppspwdngteskapdm-tsstspvttptpnatsptpavttptpnatsptp 539 320 PNTTAGQV-PTTEV-VGTTPGQAPTAEPSGTTSVQVPTTEVISTAP-VQMPTAESTGMTP 376 540 avttptpnatsptlgktsptsavttptpnatsptlgktsptsavttptpnatsptlgkts 599 377 E-KVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPE 435 421 fskapestttsptinttgfadpntttglpssthvptnltapastgptvstadvtsptpag 480 6 aptptpisttttvtptptptgtqtptttpitttttvtptptptgt---qtpttvlittt 62 Gaps 9; Gaps The donor and acceptor splice sites of the EBV gene encoding gp350/ 220 are mutated by replacement of native nucleotides by non-native gp350, useful in vaccines, is expressed in mammalian or insect cell nucleotides, without altering the encoded amino acid sequence, resulting in elimination of gp220 prodn. Recombinant homogeneous New DNA encoding a homogeneous gp350 protein — can be used for preventing and treating Epstein-Barr virus-related diseases or .; 6 EBV; qp350; qp220; qp350/qp220; non-splicing variant; vaccine. Epstein-Barr virus. Score 169; DB 14; Length 907; Pred. No. 1.32e-03; 56; Mismatches 97; Indels Score 174; DB 3; Length 278; Pred. No. 5.98e-04; 40; Mismatches 70; Indels | : ||:| |::| | 424 VET-T-ARELPIPEPEGPDASSIMST-ESITGSLGPLLDGTATL 464 121 tgppthtstapiaelttsnpppesstpqtsrstsspltesttll 164 = = = <u>:</u>: = Location/Qualifiers Disclosure; Fig.1; 61pp; English. R80144 standard; Protein; 907 AA. /note= "transmembrane region" 3.7%; Query Match 3.6%; Best Local Similarity 23.2%; 18-JAN-1996 (first entry) 49; Conservative 46; Conservative 861..881 13-APR-1995; U04611. 18-APR-1994; US-229291. Jackman WT, Spaete R; WPI; 95-373802/48. Best Local Similarity /label= Sig\_peptide Sequence 907 AA; (AVIR-) AVIRON. N-PSDB; T04821. EBV gp350/220. WO9528488-A1. 26-0CT-1995. conditions Query Match Peptide Region Matches Matches

262 FGDSSGTLISRALVVTHTYLEPGPVTA-QVVLQAAIPLTSCGSS-PVPGTTDGHRPTAEA 319 481 ttsgaspvtpspspwdngteskapdm-tsstspvttptpnatsptpavttptpnatsptp 539 320 PNITAGQV-PTIEV-VGTTPGQAPTAEPSGTTSVQVPTTEVISTAP-VQMPTAESIGMTP 376 540 avttptpnatsptlgktsptsavttptpnatsptlgktsptsavttptpnatsptlgkts 599 421 fskapestttsptlnttgfadpntttglpssthvptnltapastgptvstadvtsptpag 480 377 E-KVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPE 435 Gaps to generate antibodies reacting with the surface proteins of EBV-infected cells, and in the preparation of a vaccine against EBV. nsed 9: New fragment of Epstein-Barr Virus DNA - useful in vector to express polypeptide for use in prepn. of vaccine against the The sequence encodes an outer surface viral protein of EBV, Score 169; DB 3; Length 907; Pred. No. 1,32e-03; <del>::</del> 56; Mismatches 97; Indels Epstein-Barr virus (EBV) outer surface protein. SMUC; intestinal mucin; diagnosis; cancer. 07-AUG-1985. 28-JAN-1985, 400141. 30-JAN-1984, US-57532. 23-JUL-1984, US-633558. (WCH-) WIV OF CHICAGO. Kleff E, Tanner J, Hummel M, Belsel C. WPI; 85-191978/32. 600 ptsavttptpnatgptvgetspqanatnhtl 630 436 PEGPDASSI-MSTESITGSLGPLLDGTA-TL 464 600 ptsavttptpnatgptvgetspqanatnhtl 630 436 PEGPDASSI-MSTESITGSLGPLLDGTA-TL 464 Epstein-Barr virus; antiqen; vaccine. Claim 2; Page 23-25; 26pp; English. P50073 standard; Protein; 907 AA. R12534 standard; Protein; 166 AA virus and for use in diagnosis, 02-SEP-1991 (first entry) Query Match 3.6%; Best Local Similarity 23.2%; Matches 49; Conservative (first entry) SMUC-40 intestinal mucin. Epstein-Barr virus. N-PSDB; N50114 Homo sapiens. 17-0CT-1991 EP-151079-A. Sequence P50073; RESULT

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/note= "peptide R60"
Active_site 168..186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.5%; Score 165; DB 3; Length 166; Best Local Similarity 28.5%; Pred. No. 2.48e-03; Matches 45; Conservative 35; Mismatches 69; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence contains repeats having a threonine and proline-rich
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Herpes simplex virus; herpes virus; VP16; immediate early gene;
host cell factor; virus infection therapy; cellular protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding human intestinal mucin peptide(s) - used for producing prods. for diagnosis and treatment of disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies produced against this mucin peptide can be used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity and other glycosylation enzymes. See also Q12217-21 and Q12247-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2(A); 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1991.
04-DEC-1990; U07087.
05-DEC-1989; US-447140.
(REGC ) UNIV OF CALIFORNIA.
Kim YS, Gum JR;
WPI; 91-19314/726.
N-PSDB; Q12217.
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19-MAR-1995 (first entry)
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Modified -site 149..151
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	Active site Peptide RS2 Active site 133.340 Active site 251.526 Active site 351.526 Active site 351.526 Active site 358.594 Active site 54.611 Anote="peptide R26 list sequence"
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Disclosure; Page 39; 71pp;

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345 PSGTTSVQVPTTEVISTAPVQMPTAESTGMTPEKVPV-SEVMGTTLAEMSTPEATGMTPA 403

US-08-231-565A-27 rag

86 teq-pttdsstttesttessketpttpsteqptvd--sttpvesgttdss-va-eitpva 140 pstteseaapavtpddevkvpearvasaqtfsalsptq-spsefiaelarcaqpiaqand 199 266 SGTLISRALVVTH--TYLEPGPVTAQVVIQAAIPLISCGSSPVPGTTDGHRPTAEAPNTT 323 383 -EVMGTILAEMSTPEATGMTP-AEVSIV-VLSGTTAAQVTTTEWVETTAR-ELPIPEPEEG 438 27 sttlfssalivssvgtpvallpvtaeateeqptn-aevaqapttetglvetpttettpgi 85 Gaps and the cultures of lactic acid bacteria e.g. cheese, where the culture is production - by in situ prodn. of an auto:lysin, regulated by an a process for the lysis of a culture of lactic acid bacteria. The autolysin from a food grade Gram positive bacteria, can be used In situ production of a homologous autolysin or a heterologous Lysin; autolysis; culture; lactic acid bacteria; fermentation; cheese; foodstuffs; induction. lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added an lysin does not need to be isolated or encapsulated. The time lysis can be precisely controlled. This is the Streptococcus process can be used in the manufacture of products containing Length 671; Lysis of a culture of lactic acid bacteria in, e.g. cheese Venema G; Disclosure; Page 66-69; 103pp; English. 161 matmaatatltmaaraamaaraettt 186 :: : | ||: : : |||: 404 EVSIVVLSG-TTAAQVTTTEWVETTA 428 Streptococcus faecalis autolysin. LT 15 R75107 standard; Protein; 722 AA. R75107; R85290 standard; Protein; 671 AA. Ledeboer AM, 3.2%; Local Similarity 28.2%; (first entry) 55; Conservative 200 lyas-vmmagaives 213 439 PDASSIMSTESITGS 453 Streptococcus faecalis. 12-MAY-1995; NL0170. 12-MAY-1994; EP-201353. (UNIL ) QUEST INT BV faecalis autolysin. inducible promoter. Buist G, Kok J, I WPI; 96-010946/01. <u>::</u> :: :: :: WO9531561-A1. 02-APR-1996 23-NOV-1995. Sequence Query Match Matches 141 RESULT 임 à 임 à 유 δ g 8 В Š 16; 7; 433 aapavqpltqvgitllpqaapappttttiqvlpt-v-pgssisvptaartqgvpavlkvt 490 491 gpgattgtplvtmrpasgagkap--vtvtslp-agvrmvvptgsaggtvig-sspgmsgm 546 43; Mismatches 58; Indels 7; Gaps 46 amtvavttavvvtmaa-aattvvaatmavaatmavaattvv-aattavv-ttmavaattv 102 285 PVTAQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPTAE 344 103 vaatmavav-ttvvaatmavaattvvaatmavaaitvvaatmaatmavimaettat-maat 160 376 ntnslevswgavatadsyllqlq-kydipataata-tsptpnpvpsvp-anppkspapaa 432 323 TAGQVPTTEVVGTTPGQAPTAEPSGTTSVQVPTTEVISTAPVQMPTAEST-GMTPE-KVP 380 Gaps associate with HCF or designing compounds capable of modifying HCF transcription. Such agents can be used to treat viral infections. for preparing poly-hydroxy-alkanoate in large quantities Claim 3; Page 10-11; 15pp; Japanese. R53915 is encoded by ORF 1 of Q63789, which produces a polypeptide which shows polyhydroxyalkanoate decomposing activity. The method HCF is required for the transcription of a number of viral genes, such as the immediate early herpes simplex virus-1 DNA encoding poly-hydroxy-alkanoate decomposing enzyme - useful used allows the polypeptide to be prepared in large quantities. Sequence 252 AA; defining functional domains of HCF, identifying compounds that Score 162; DB 11; Length 2035; Pred. No. 3.97e-03; 53; Mismatches 85; Indels 17; 3.3%; Score 157; DB 10; Length 252; 26.0%; Pred. No. 8.66e-03; Epitopes of the encoded protein can be used in polypeptide. (CHIK-) 2H CHIKYU KANKYO SANGYO GIJITSU KENKYU, Polyhydroxyalkanoate decomposing activity po Polyhydroxyalkanoate decomposing enzyme; PHA : |:: :| | :| | :| 439 PD-ASSIMSTESITGSLGP-LLDGTATLRLVK 468 547 aalaaaaaatqkippssaptvlsvpagttivk 578 R53915 standard; Protein; 252 AA. (ELED ) DENKI KAGAKU KOGYO KK. (UYKA-) GH KANAGAWA DAIGAKU Query Match 3.4%; Best Local Similarity 26.9%; Best Local Similarity 26.0%; 57; Conservative (first entry) 38; Conservative 07-SEP-1992; JP-279099. 07-SEP-1992; 279099. 2035 AA; WPI; 94-140539/17. N-PSDB; Q63879. Zoogloea ramigera. 07-DEC-1994 J06086681-A. 29-MAR-1994. Sequence Sequence Query Match denes. Matches Matches

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01-FEB-1996 (first entry)

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Score 147; DB 14; Length 722;
Pred. No. 4.05e-02;
50; Mismatches 67; Indels 12; Gaps 12;
                                                                                                                                                                                                                                                                                                                               Disclosure; Pagaring; Inpp, Japanese.

New lipases are ones in which 1-15 repeats of any of the sequences RY509-RY5105 (encoded by Q90570-Q90576) are attached to the C-terminus of the bile salt-activated lipase (BAL) of sequence RY5098 (encoded by Q90569) and/or in which the amino acid sequence SMTGS (encoded by Q90578) is attached to the N-terminus of the BAL. The recombinant lipases can be produced by fermentation in Pichia pastoris GS 115 transformed host cells. The present sequence is a protein with 16 copies of the undecapeptide imperfect repeats at the BAL C-terminus.

Sequence 722 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant bile salt-activated lipase(s), DNA encoding them and vectors - useful for high level expression of the lipase(s) by fermenter-culturing.
             Bile salt-activated lipase with 16 C-terminal 11-mer repeats.
Bile salt activated lipase; BAL; C-terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660 pvpptgdsgappvtptgdsetapvpptgdsg-appvpptgdseaapvpptd 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 GMTPA-EVSIVVLSGTTAAQVTTTEMVETTARELPIPEPEGEDBASSIMSTE 448
                                                                                                   /note= "contains 16 copies of imperfect 11mer repeats; the region is made up from a combination of 7 different sequences"
                                                                   Location/Qualifiers
539..722
                                                                                                                                                                                                                        (MEIP ) MEIJI MIIK PROD CO LTD. WPI; 95-196318/26. N-PSDB; Q90579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.1%;
Best Local Similarity 24.6%;
Matches 42; Conservative
                                                                                                                                                                                                           30-SEP-1993; JP-245079.
                                                                                                                                                                          02-MAY-1995.
30-SEP-1993; 245079.
                                                                                                                                                           J07111891-A.
                                                      Mammalia.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Tue Aug 27 08:10:55 1996; MasPar time 25.85 Seconds 650.166 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-231-565A-27 (1-661) from US08231565A.pep 4698

Description: Perfect Score:

1 MDIVLKRCLLHLAVIGALLA.....RIFCSCPIGENSPLLSGQQV 661 Sequence:

PAM 150 Gap 11 Scoring table:

82130 seqs, 25426960 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir47

14:unrev

Mean 50.761; Variance 151.386; scale 0.335

Statistics:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Query Score Match Length DB	ngth		80	8	Description	Pred. No.
· i	וואכוו חם	3	•	10	Description	rreg. No.
7.66	661 11	11		A53668	glycoprotein gp100 p	
97.8	668 11	11		A41234	melanocyte-specific	
63.9	626 12	12		553871	Pmel 17 protein - mo	
54.1	491 12	12		A49179	melanoma antigen hom	_
4.6	873 14	14		A47283	calphotin - Drosophi	~~
4.5	294 11	Ξ		A37232	mucin, tracheal (AMN	2.97e-10
4.4	400 5	S		A28172	spasmolysin precurso	•
4.4	865 10	12		A47282	calcium-binding prot	
4.3	447 12	12		A39321	mucin - rat (fragmen	•
4.2	322 12	12		A53715	apomucin precursor -	_
183 3.9 279 11	279 11	1		553363	mucin JER58 - human	4.91e-07
3.7	167 11	Ξ		A33532	mucin SMUC-40 - huma	3.56e-06

7.43e-06	1.54e-05	1.54e - 05	2.50e - 05	2.50e - 05	6.55e-05	5.16e-05	16e-	5.16e - 05	6.55e-05	1.06e - 04	1.34e - 04	1.34e - 04	8.32e-05	8.32e-05	3.45e - 04	4.37e-04	1.40e - 03	2.22e-03	2.22e-03	1.76e - 03	1.76e - 03	1.11e-03	1.76e - 03	5.54e - 03	5.54e-03	54e-	5.54e-03	2.79e - 03	•	8.72e-03	8.72e-03
probable arabinogala		membrane antigen gp3	probable membrane pr	glucan 1,4-alpha-glu	mucin - rat	mucin (clone PGM-2A)	mucin - human (fragm	spore coat protein S	mucin - human (fragm	mucin like protein M	mucin, MG2=low molec	glycoprotein 350/220	Cl factor precursor	HCF, C1, VCAF, CFF=V	mucin FIM-C.1 - Afri	sialidase - Actinomy		hypothetical protein	autolysin - Enteroco	transcription factor	transcription factor	mucin, tracheobronch	mucin 2, intestinal/	larval glue protein	glue protein lgp-1 -	TPX-VT3 -	m	triacylglycerol lipa	protein -	mucin 4, tracheal -	shed acute-phase ant
S55925	VGBEX1	QQBE21	S57180	S48478	S24169	S55315	A43932	507638	A45106	PC2022	A48018	529605	A56088	A40718	A45155	A49227	<b>S55316</b>	F36791	A38109	A34873	A47001	A48292	A54895	A60095	S50126	989908	<b>S15921</b>	<b>S13586</b>	<b>S53720</b>	PN0012	223006
215 9	797 3	907 3	1161 10	1367 4	292 12	528 12		6 009	1270 14	235 12	377 11	9 988	2035 11		662 11		317 12	9 0/9	671 8	739 6	9 991	1118 12	1513 12		232 11		474 6		377 12	610 11	879 10
3.7	. 6	3.6	3.6	3.6	3.5	3.5	3.5	3.5	3.5	3.4	3.4	3.4	3.4	3.4	3.3	3,3	3.2	3.2	3.2	3.2	3.2	3.5	3.2	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0
172	169	169	167	167	163	164	164	164	163	161	160	160	162	162	156	155	150	148	148	149	149	151	149	144	144	144	144	147	142	142	142
13	15	. 16	11	18	19	70	21	22	23	24	52	56	27	88	59	30	31	32	33	34	35	36	31	38	39	40	41	42	43	44	45

#### ALI GNMENTS

A53668 #type complete glycoprotein gp100 precursor, melanocyte lineage - human s melanoma antigen 25 #formal name Homo sapiens #common_name man 07-oct-1994 #sequence_revision 07-oct-1994	A53668; A55753 A53668 Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.	J. Biol. Chem. (1994) 269:20126-20133 Molecular characterization of the melanocyte lineage-specific antigen gp100. A53668 le type mRNA	#fresiduss 1-61 ##label ADE NCE A55153 thors Kawakami, Y.; Eliyahu, S.; Delgado, C.H.; Robbins, P.F.; askaguchi, K.; Appella, E.; Yannelli, J.R.; Adema, G.J.; Miki, T.; Rosenberg, S.A.	Proc. Natl. Acad. Sci. U.S.A. (1994) 91:6458-6462 Identification of a human melanoma antigen recognized by tumor-infiltrating lymphocytes associated with in vivo tumor rejection.	A55753 not compared with conceptual translation
RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE	ACCESSIONS REFERENCE #authors	<pre># journal #title #accession ##molecul</pre>	##residue REFERENCE #authors	#journal #title	#accession ##status

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Query Match

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181 181 241 241

##note

KEYWORDS SUMMARY

cross-references MUID:92021023 preliminary 97.8%; 98.7%; Best\_Local Similarity 98.7%, Matches 659; Conservative 30-Sep-1993 A41234 ##status #accession Query Match **f**authors journal ACCESSIONS 181 181 241 241 301 361 title 301 361 481 541 541 421 481 601 REFERENCE 421 SUMMARY 염 Š g à 셤 ò 8 5 g ð 엄 ð g ð g g ò qq ð 9 δ ö 120 120 180 240 240 300 300 9 009 099 121 VYPQETDDACIFPDGGPCPSGSWSQKRSFVYVWKTWGQYWQFLGGPVSGLSIGTGRAMLG 180 tapvçmptaestgmtpekvpvsevmgttlaemstpeatgmtpaevsivvlsgttaaqvtt 420 tewvettarelpipepegpdassimstesitgslgplldgtatlrlvkrqvpldcvlyry 480 099 9 9 Gaps melanocyte-specific protein Pmel-17 precursor - human #formal name Homo sapiens #common name man 19-Jun-1992 #text\_change 61 WRGGQVSIKVSNDGPTLIGANASFSIALNFPGRGKVIPUTITITITITINGSQVAGGQP vypqetddacifpdggpcpsgswagkrsfvyvwkkwgqywqvlggpvsglsigtgramlg wrggqvslkvsndgptliganasfsialnfpgsqkvlpdgqviwvnntiingsqvwggqp thtmevtvyhrrgsrsyvplahsssaftitdqvpfsvsvsqlraldggnkhflrnqpltf alqlhdpsgylaeadlsytwdfgdssgtlisralvvthtylepgpvtagvvlgaaiplts mdlvlkrc1lhlavigallavgatkvprnqdwlgvsrqlrtkawnrqlypewteagrldc 1 MDLVLKRCLLHLAVIGALLAVGATKVPRNQDWLGVSRQLRTKAWNRQLYPEWTEAQRLDC . #checksum 661 Indels Length #molecular-weight 70255 DB 11; Score 4684; DB 11; Pred. No. 0.00e+00; 1-161,'F',163-661 ##label KAW nucleotide sequence not given 0; Mismatches #type complete 99.7**%**; 99.8**%**; 660; Conservative glycoprotein #length 661 mRNA. Best Local Similarity ##molecule\_type ##residues

301 361 361 421

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v 661 661

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541 601 601 661 661

421 481 481 >

RESULT ENTRY TITLE ORGANISM

US-08-231-565A-27.rpr Aug 27 08:00 C.A.; Copeland, N.G.; 240 240 300 420 420 480 540 61 WRGGQVSLKVSNDGPTLIGANASFSIALNFPGSQKVLPDGQVIWVNNTINGSQVWGGQP 120 300 360 360 480 540 9 593 099 61 wrggqvslkvsndgptliganasfsialnfpgsqkvlpdgqviwvnntiingsqvwggqp 120 ailver 9 8 Gaps thtmevtvyhrrgsrsyvplahsssaftitdqvpfsvsvsqlraldggnkhflrnqpltf tapvqmptaestgmtpekvpvsevmgttlaemstpeatgmtpaevsivvlsgttaaqvtt TAPVOMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTT gsfsvtldivqgiesaeilqavpsgegdafeltvscqgglpkeacmeisspgcqppaqrl -----GQEAGL 1 mdlvlkrcllhlavigallavgatkvprngdwlgvsrglrtkawnrglypewteagrldc cqpvlpspacqlvlhqilkggsgtyclnvsladtnslavvstqlimpvpgilltgqeagl gqvplivgillvlmavvlasliyrrrlmkqdfsvpqlphssshwlrlprifcscpigens ##cross-references GB:M77348 Y #length 668 #molecular-weight 70932 #checksum 6409 A melanocyte-specific gene, Pmel 17, maps near the s coat color locus on mouse chromosome 10 and is in Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copelanc Gilbert, D.J.; Jenkins, N.; Barton, D.; Francke, ; Proc. Natl. Acad. Sci. U.S.A. (1991) 88:9228-9232 Length 668 Indels syntenic region on human chromosome 12 2; Score 4595; DB 11; Pred. No. 0.00e+00; 0; Mismatches Kobayashi, Y.; Kim, K.K. ##molecule\_type mRNA ##residues 1-668 ##label KWO

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Qy 594	GQVP-LIVGILLVILMAVVLASTIYRRRLMKQDFSVPQLPHSSSHWLRLFRIFUSCFIGENS 65
Db 661	pllsgggv
Oy 654	
RESULT ENTRY TITLE ORGANISM DATE	3 S53871 #type complete Pmel 17 protein - mouse 1 #formal name Mus musculus #common_name house mouse 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
REFERENCE #authors #journal #title	
#acce ## ## SUMMARY	#actession 5538H preliminary ##status preliminary ##molecule_type mRNA
Query M. Best Lo Matches	Match Local Similarity 72.6%; Pred. No. 0.00e+00; Les 480; Conservative 70; Mismatches 76; Indels 35; Gaps 12;
Db Qy	<pre>1 mvgvqrrsflpvlvlsallavgalegsrnddwlgvprqlvtktwnrdlypewtevggsnc 60</pre>
9 40 9 40	61 wrggqvslrvindgptlvganasfsialhfpgsqkvlpdgqviwanntiingsqvwggqp 120 
0b 121 Qy 121	<pre>1 vypqepddacvfpdggpcpsgpkppkrsfvyvwktwgkywqvlggpvsrssiatnhaklg 180</pre>
Db 181 Qy 181	1 thtmevtvyhrrgagsyplahasstftitdqvpfsvsvsqlqaldgetkhflrnhplif 240 
Db 241 Qy 241	1 alqihdpsgylaeadlsytwdfgdgtgtlisraldythtylesgsytagyvlqaaiplys 300 
Db 301 Qy 301	1 cgsspvpgttdgymptaeapgttsrggtttkvvgttpgdmpttgpsgttvvqmpttevta 360 
Db 361 Qy 361	ttseqm  tsa-v- -dtt  aevsttegtgttptr-psgttvaqa 400  ::
Db 401 Qy 421	1 tttegpdaspllptqsstgsispllddtdtimlvkrqvpldcvlyry 447 
Db 448	8 gsfelaldivqgiesaeilqavpfsegdafeltvscqgglpkeacmdisspgcqppaqrl 507     ::

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qa	P 208	cgsvppspdcglvlhqvlkggsgtyclnvsladanslavastqlvvpgddgglgqapllv 567
δλ	у 541	
ΩP	b 568	
ρŷ	у 601	GILLVIAMAVVIASLIYRRRIAMKQDFSVPQLPHSSSHWIRIPRIFCSCPIGENSPLISGQQ 660
qq	b 626	v 626
δ	у 661	V 661 .
<b>2</b>	RESULT	T T
a ⊧	ENTRY	A49179 #type iragment melanoma antigan homolog rred - bowine (fragment)
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	#journal #title	3 £
		products preferentially expressed in retinal pigme epithelium.
	#cros	cross-references MUID: 9312163
	#acce#	A4917
	* *	##status ##molecule_type nucleic acid
	* *	##residues 1-491 ##label KIM ##cross-references NCBIN:122438; NCBIP:122439
	****	##experimental source retinal pigment epithelium
SI	**I SUMMARY	##Note sequence extracted from Nubl backbone Y #length 491 #checksum 3125
	Query 1	Query Match 54.1%; Score 2541; DB 12; Length 491;
ě	Best Lo Matches	
qq		qywqvlggpvsgleigtdkamlgtynmevtvyhrrgsqsyvplahsseaftitdqvpfsv 60
Qy	y 158	
qa	b 61	svsqiqaldgrnkrfirkqpitfalqlhdpsgylagadlsyt#dfgdstytlisraltvt 120
Qy	у 218	
qu	ь 121	
Q	y 278	HYLEPGEVTAQVVIQAAIPLTSCGSSPVPGTTDGRRPTAEAPNTTAGQVPTTEVVGTTP 337
ସ୍	b 181	ggvptaeapgttvgwvpttedvgttpeqvatskvlsttpvemptaka 227
δ	y 338	
qq	b 228	
٥y	y 398	TCMTPAEVSIVVLSGTTAAQVTTTEMVETTARELPIPEPEGPDASSIMSTESITGSLGPL 457
qq	5 287	pddtatlylekrqapldcylyrygsfsltldiv-siesaeilqavsssegdafeltvscq 345

NNS A37232 CE A37232 CE A37232 Inal J. Clin. Inv le The core pol contains a mucin in a ss-references MUID:910 ession A3732 #status #molecule_type_mNNA #residues #cross-references GB:M #cross-references GB:M #cross-references GB:M	COMENTALY  Query Match  Query Match  Query Match  Query Match  Query Match  Beet Local Similarity 26:54, Score 212, DB 11; Length 294;  Beet Local Similarity 26:54, Fred. No. 2.97e-010  Beet Local Similarity 26:54, Fred. No. 2.97e-010  Beet Local Similarity 26:54, Fred. No. 2.97e-010  De 16 pittittmutpippitstqptppitttttptptptptstqttptatttttvtptptp 75	#label SPG\ 74-114 #domain trefoil homology #label TRF2\
Qy         458 IDGTATIRLVKRQVPLDCVLYRYGSFSVTLDIVQGIESAEILQAVPSGEGDAFELTVSCQ 517           Db         346 gglpkeacmdisspgcqlpaqrlcqpvpspacqlvlhqvlkggsqtyclnvsladansl 405           ill	te  avision 21-Sep-1993 #  svision 21-Sep-1993 #  1. Harshman, K.D.  1. S.A. (1993) 90:1536  tor cell-specific protains a leucine zippe from NCBI backbone weight 85445 #check from NCBI backbone weight 85445 # flodels smatches 78; Indels smatches 78; Indels smatches 78; Indels sasptpaavtpvvspviatpp :::        :     SCGSSPVPGTTDGHRPTAEAP reetpapppvaeipvatipec ::        :     SCGSSPVPGTTDGHRPTAEAP stantyOMPTAE-STGMTPER sphvsvapavetavva-pvsa ::  :       :     AQVTTTEMVETTARELPIPE  at Formmon name man svision 14 Feb-1993 #	DAIE 14-teD-1992 #sequence_revision 14-reD-1992 #text_cnange 30-Sep-1993

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5-18-231-56	
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IS-118-231-565	
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; #region 9-residue repeats (D/E-T-T-T-A-S-T-T-A)\
#region 9-residue repeats (E-T-T-T-V-P-T-T-P)\
#region 4-residue repeats (E-T-T)\
#domain trefoil homology #label TRF3\
#domain trefoil homology #label TRF3\
#domain trefoil homology #label TRF3\ 122 pdtttasttaetttvpttpetttvpttpetttvpttpetttvpttpetttvpttp-ettt 180 283 PGPVTAQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPT 342 181 v-pttpetttvpttpetttvpt-tpetttvpttpetttvpttpetttvp-ttpetttast 237 #binding site carbohydrate (Asn) (covalent) #status 7; Gaps predicted #length 400 #molecular-weight 42641 #checksum 1484 238 taetttvpttpettteptttpttdttpptlp-ptpetttetttetttet 289 Score 206; DB 5; Length 400; Pred. No. 1.41e-09; 34; Mismatches 80; Indels #disulfide\_bonds #status predicted\ fregion PEST\ Query Match 4.4%; Best Local Similarity 30.1%; 52; Conservative 23-49, 33-48, 43-60, 74-100, 84-99, 94-111, 312-327, 322-339, 353-379, 363-378, 373-390 123-131, 231-239 132-230, 240-248 249-252, 276-299 351-400 353-393 305-342 Matches SUMMARY g g q δ ò

RESULT ENTRY

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Calphotin: a Drosophila photoreceptor cell calcium-binding calcium-binding protein calphotin - fruit fly (Drosophila 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995 Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A. Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1531-1535 formal name Drosophila melanogaster #type complete cross-references MUID:93165729 preliminary melanogaster) protein A47282 A47282 A47282 A47282 ##status #accession **fauthors** | journal ACCESSIONS title REFERENCE ORGANISM TITLE DATE

##cross-references NCBIN:124955; NCBIP:124956 ##molecule\_type nucleic acid ##residues 1-865 ##label MAR

6 4.4%; Score 205; DB 10; Length 865; Best Local Similarity 23.7%; Pred. No. 1.83e-09; Matches 47; Conservative 63; Mismatches 79; Indels Query Match SUMMARY

114 vappvaatptpvvqipvaapvi--atppvaasaptpaavtpvispviasppvvpanttvp 171 음 ð

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386 GTILAEMSTPEATGMTPAEVSI-VVLSGTTAAQVTTTEWVETTARELPIPEP-EGPDASS 443 232 vvatkplaaaepvvvappatetpvvapaaasphvsvapavetavva-pvsasteppvaaa 290 329 ITEVVGTTPGQAPTAEPSGTTSVQVPTTEVISTAPVQMPTAE-STGMTPEKV-P-VSEVM 385 172 vaapvaavpaavpvvapvlapavapavapvvaetpapppvaeipvatipecvaplipevs 231 mucin - rat (fragment) #formal name Rattus norvegicus #common name Norway rat 19-Jun-1992 #text\_change Gum Jr., J.R.; Hicks, J.W.; Lagace, R.E.; Byrd, J.C.; Toribara, N.W.; Siddiki, B.; Fearney, F.J.; Lamport of Lack Length 447; Molecular cloning of rat intestinal mucin. conservation between mammalian species. J. Biol. Chem. (1991) 266:22733-22738 ##cross-references GB:M76740 Y #length 447 #checksum 7414 #type fragment 1-447 ##label GUM D.T.A.; Kim, Y.S. cross-references MUID:92042224 preliminary 291 tlttapetpalapvvaes 308 444 IMSTESITGSLGPLLDGT 461 18-Jun-1993 ##molecule\_type mRNA A39321 A39321 A39321 A39321 ##residues ##status #accession 6 **authors** journal ACCESSIONS title TITLE ORGANISM REFERENCE SUMMARY RESULT ENTRY δ 염 Š 임 Š

Gaps 46; Mismatches 64; Indels 10; Query Match 4.3%; Score 200; DB 12; Best Local Similarity 29.0%; Pred. No. 6.63e-09; Matches 49; Conservative 46; Mismatches 64

10;

199 vt-tta-dvtttasvtttp-dvtttpdvtttpd-vtttagvtttpdatttpdatt-tp-q 252 139 vtttvdvtttvdvtttaevttttevttspdattttdvtttpeatttdgvtttpdvtttsd 198 286 VTAQVVIQAAIPLISCGS-SPVPGTIDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPTAE 344 g ð 셤

345 PSGTTSVQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAE 404 ð

253 vttta-dvtttagvtttagv-tttpdvttt-pdvtttpdvtttasvttt 298 염 ð

#formal name Rattus norvegicus #common name Norway rat 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change #type complete apomucin precursor - rat A53715 ORGANISM ENTRY DATE

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A53715 #authors #journal ACCESS IONS REFERENCE

Albone, E.F.; Hagen, F.K.; VanMuyckhuyse, B.C.; Tabak, L.A. J. Biol. Chem. (1994) 269:16845-16852
Molecular cloning of a rat submandibular gland apomucin. A53715 #accession #title

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Guyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.;
Buisine, M.P.; Galiegue-Zouitina, S.; Pigny, P.; Degand,
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                                                                                                                                        #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                         306 VPGTIDGHRPIAEAPNTIAGQVPTIEVVGTIPGQAPIAEPSGTISVQVPTIEVISTAPVQ 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||::|| :| :| :| :: :::| ::| ::| 366 MPTAESTGMTPEKVPVSEVMCTTLAEMSTPEATGMTPAEVSIVULSGTTAAQVTTTEMVE 425
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#length 322 #molecular-weight 34975 #checksum 1086
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Pred. No. 4.91e-07;
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Pred. No. 1.11e-08;
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                                             1-322 ##label ALB
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Best Local Similarity 26.9%;
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402 PAEVSIVVISGTTAAQVTTTEMVETTARELPIPEPEGPDASSIMSTESITGSLGPLLDGT 461

7; Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. (1989) 264:6480-6487
Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evidence for genetic polymorphism. Characterization of a cDNA encoding the protein moiety of a putative arabinogalactan protein from Lycopersicon 68 gtqtptttpitttttvtptptptgtqt-ptptp-itttttv-tptptptg-tqtptptpi 123 265 SSGTLISRALVVTHT-YLEPGPVTAQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTT 323 324 AGQVPTTEVVGTTPGQAPTAEPSGTTSVQVPTTEVISTAPVQMPTAESTGMTPEKVPVSE 383 9 stttmvtptptptgtqtltptpittttv-tptptptgtqtptstpisttttvtptptpt 67 probable arabinogalactan protein precursor - tomato #formal\_name Lycopersicon esculentum #common\_name tomato 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change Gaps #formal\_name Homo sapiens #common\_name man 29-Jan-1990 #sequence\_revision 27-Jun-1994 #text\_change 27-Jun-1994 ##cross-references EMBL:247980 flength 215 #molecular-weight 20812 #checksum 3703 7; Length 167; 36; Mismatches 71; Indels Score 175; DB 11; Pred. No. 3.56e-06; Pogson, B.J.; Davies, C. Plant Mol. Biol. (1995) 28:347-352 124 tttttvtptptptgt-qtptstpittnttvtptptpt 159 384 VMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTT 420 nucin SMUC-40 - human (fragment) #length 167 #checksum 7137 #type fragment #type complete 1-215 ##label POG 1-167 ##label GUM ##cross-references GB:M22404 #cross-references MUID:89197956 preliminary Query Match 3.7%; Best Local Similarity 27.4%; Matches 43; Conservative 03-Nov-1995 glycoprotein esculentum. ##molecule\_type mRNA ##molecule type mRNA A33532 A33532 S55925 S55925 \$55925 A33532 S55925 ##residues ##status accession #accession 12 #authors | journal authors journal ACCESSIONS ACCESSIONS title REFERENCE TITLE ORGANISM title REFERENCE ORGANISM KEYWORDS SUMMARY SUMMARY RESULT RESULT ENTRY TITLE ENTRY DATE 염 Š 셤 g δ à

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RESULT ENTRY

glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p) #domain signal sequence #status predicted #label SIG\
#product glycoprotein X #status predicted #label MAT\
#region serine/threonine-rich\ 51 sspttssppttssspptsthtsspsststqssstaatsssapstassttsiptststettt 110 283 PGPVTAQVVLQAAIPLISCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVGTTPGQAPT 342 111 ttptastttpttttaapttaatttavttaastsaetttatat-atstpttttptstttt 169 : |:::|: || :||: || | | || 343 AEDSGTISVQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTP 402 | :: ::||: |:: ::|
403 AEVSIVVLSGTTARQUTTTEMVETTARELPIPEPECPDASSIMSTESITGSLGPLLDGTA 462 Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. submitted to GenBank, March 1992 Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. Virology (1992) 189:304-316 #binding site carbohydrate (Asn) (covalent) #status #domain transmembrane #status predicted #label TMN\ Gaps #domain equine herpesvirus 1 glycoprotein homology #formal\_name equine herpesvirus 1
host Equus caballus (domestic horse)
30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change
17-Feb-1995 #superfamily equine herpesvirus glycoprotein X; equine annotation; possible protein-coding frames neither amino acid nor nucleotide sequence is given Score 169; DB 3; Length 797; Pred. No. 1.54e-05; 64; Mismatches 84; Indels 1; #length 797 #molecular-weight 80342 #checksum #title The DNA sequence of equine herpesvirus-1. #cross-references MUID:92295566 | : ||:| :::: || :: || 424 VET-T-ARELPIPEPEGPDASSIMST-ESITGSLGPLLDGTATL 464 121 tgppthtstapiaelttsnpppesstpqtsrstsspltesttll 164 The DNA sequence of equine herpesvirus-1 herpesvirus 1 glycoprotein homology glycoprotein; transmembrane protein #type complete 1-797 ##label TEL #label EHG\ ##cross-references GB:M86664 predicted Query Match 3.6%; Best Local Similarity 17.7%; 32; Conservative ##molecule\_type DNA H36802

v Search completed: Tue Aug 27 08:12:37 1996
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Tue Aug 27 08:09:36 1996, MasPar time 16.82 Seconds 683.056 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-231-565A-27 (1-661) from US08231565A.pep 4698 Description: Perfect Score: Title:

1 MDLVLKRCLLHLAVIGALLA.....RIFCSCPIGENSPLLSGQQV 661 Sequence:

PAM 150 Gap 11 Scoring table:

49340 seqs, 17385503 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries Database:

swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Mean 52.781; Variance 121.768; scale 0.433

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	a	Description	Pred. No.
-	4586	97.6	1	9	PM17 HUMAN	PMEL 17 PROTEIN PRECU	0.00e+00
2	206	4.4		'n	MUA1 XENLA	INTEGUMENTARY MUCIN A	6.74e-13
m	205	4.4		7	CPN DROME	CALPHOTIN.	9.36e-13
4	169	3,6		<b>∞</b>	VGLX HSVEB	GLYCOPROTEIN X PRECUR	8.77e-08
5	169	3.6	907	œ	VGP3 EBV	ENVELOPE GLYCOPROTEIN	8.77e-08
9	167	3.6	1367	-	AMYH YEAST	GLUCOAMYLASE S1/S2 PR	1.62e-07
7	164	3.5	009	-	SP96_DICDI	SPORE COAT PROTEIN SP	4.02e-07
00	163	3.5	2274	2	MUC2_HUMAN	MUCIN 2 (INTESTINAL M	5.44e-07
6	156	3,3	662	S	MUC1 XENLA	INTEGUMENTARY MUCIN C	4.41e-06
10	148	3.2	670	œ	VG50 HSVI1	HYPOTHETICAL GENE 50	4.58e-05
11	148	3.2	671	-	ALYS ENTFA	AUTOLYSIN (EC 3.5.1.2	4.58e-05
12	149	3.5	739	9	OCT1 CHICK	OCTAMER-BINDING TRANS	3.43e - 05
13	149	3.2	743	9	OCT1 HUMAN	OCTAMER-BINDING TRANS	3.43e - 05

1.44e-04	6.11e-05	1.09e-04	3.38e - 04	3.38e-04	2.55e-04	3.38e - 04	4.48e - 04	7.84e-04	1.04e - 03	1.37e-03	1.04e - 03	2.37e-03	7.84e-04	4.09e - 03	4.09e-03	4.09e-03	7.04e-03	7.04e-03	5.37e-03	1.20e-02	9.21e-03	2.05e - 02	9.21e-03	1.57e-02	1.57e-02	4.51e-02	4.51e-02	3.47e-02	3.47e - 02	4.51e-02	4.51e-02
VIRAL PROTEIN TPX.	BILE-SALT-ACTIVATED L	HYPOTHETICAL 133.5 KD	HYPOTHETICAL 24.1 KD	APOPOLYSIALOGLYCOPROT	MUCIN 4 (TRACHEOBRONC	HYPOTHETICAL 84.3 KD	S-LAYER PROTEIN (PARA	INTEGUMENTARY MUCIN B	CHITINASE 3 PRECURSOR	HYPOTHETICAL 63.8 KD	GLYCOPROTEIN G.	ENDOGLUCANASE PRECURS	A-AGGLUTININ ATTACHME	HAM34 PROTEIN.	MEROZOITE SURFACE PRO	SYNDECAN-3 (N-SYNDECA	PIR3 PROTEIN PRECURSO	CELL SURFACE ANTIGEN	MUCIN 1 PRECURSOR (PO	LEUKOSIALIN PRECURSOR	TRANS-ACTING TRANSCRI	HYPOTHETICAL 166.0 KD	IMMUNOGLOBULIN A1 PRO	CELLULOSOMAL SCAFFOLD	CREB-BINDING PROTEIN.	SED1 PROTEIN PRECURSO	SKIN SECRETORY PROTEI	GLUCOSE REPRESSION RE	GLUCOAMYLASE S1 PRECU	APOMUCIN (MUCIN CORE	SIALIDASE (EC 3.2.1.1
VTP3 TTV1V	BAL HUMAN	YQU3 CAEEL	Y091 NPVAC	PSGL_ONCMY	MUC4 HUMAN	YS8A CAEEL	SLAP CAUCR	MUB1 XENLA	CHI3 CANAL	YHC8 YEAST	VGLG_HSV2	GUN6 DICDI	AGA1 YEAST	HA34 BRELC	MSP8 EIMAC	SDC3_RAT	PIR3 YEAST	C114 MOUSE	MUC1 MOUSE	LEUK HUMAN	ICPO_HSVBJ	YCX9 YEAST	IGA4 HAEIN	CIPA CLOTM	CBP MOUSE	SEDI YEAST	XP2 XENLA	TUP YEAST	AMYH SACDI	APMU_PIG	TCNA_TRYCR
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3.1	3.1	3.1	3.0	3.0	3.0	3.0	3.0	5.9	2.9	5.9	5.9	2.9	2.9	2.8	5.8	2.8	5.8	2.8	5.8	2.7	2.1	2.7	2.7	2.7	2.7	5.6	5.6	5.6	5.6	5.6	5.6
144	147:	145	141	141	142	141	140	138	137	136	137	134	138	132	132	132	130	130	131	128	129	126	129	127	127	123	123	124	124	123	123
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

							EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					N.G.,	GILBERT D.J., JENKINS N., BARTON D., FRANCKE U., KOBAYASHI Y.,		•	-!- FUNCTION: COULD BE A MELANOGENIC ENZYME.	IN MELANOCYTES.	<ul><li>-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).</li></ul>			TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; MELANIN BIOSYNTHESIS; REPEAT.				
668 AA.		E)	OATE)				TETRA					COPELAN	VCKE U.		32 (1991)	Œ.	(PRESSE)	E PROTE			NIN BIO		EIN.		
668		UPDA	IAN NC				3RATA;					.A.,	FRA		28-95	ENZ	CI X	BRANE			, MEL	IAL.	PROJ	[AL.	IAL.
PRT;	ED)	SEQUENCE	ANNOTATIO				A; VERTEI					KOZAK C	ARTON D.,		A. 88:92;	LANOGENI	FERENTIAL	YPE I MEN			; SIGNAL,	POTENTIAL.	PMEL 17 PROTEIN.	POTENTIAL.	POTENTIAL.
В <b>Э</b> ;	CREAT	LAST	LAST	RSOR.			HORDAT					NI C.,	N., B		. 0.5.	EAME	Y: PRE	ION: T		rion.	ROTEIN	m	m		<b>м</b>
STANDARD;	. 31,	31,	31,	RECU		(MAN)	)A; C	د	•	<u></u>	~·	MANE	KINS		SCI	10 B	TICIL	OCAT	7348.	EDI	YCOP	23	999	595	623
S.	(REL	(REL	(REL	EIN		<b>E</b>	ETAZ(	IMAT		N W	21023	HINT	B		ACAD	8	PECIF	ILAR I	1, M7	1111	E; G	-	24	575	603
JLT 1 PM17 HUMAN PA1957.	01-FEB-1995 (REL. 31, CREATED)	01-FEB-1995	01-FEB-1995	PMEL 17 PROTEIN PRECURSOR.	PMEL17.	HOMO SAPIENS (HUMAN).	EUKARYOTA; M	EUTHERIA; PRIMATES.	Ξ	SEQUENCE FROM N.A.	MEDLINE; 92021023.	KWON B.S., CHINTAMANENI C., KOZAK C.A., COPELAND N.G.,	GILBERT D.J.	KIM KK.;	PROC. NATL. ACAD. SCI. U.S.A. 88:9228-9232(1991).	-!- FUNCTION	- i- TISSUE S	-;- SUBCELLU	EMBL; M77348; M77348.	MIM, 155550, 11TH EDITION.	TRANSMEMBRAN	SIGNAL	CHAIN	TRANSMEM	TRANSMEM
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RESULT

-!- PTM: EXTENSIVELY O-GLYCOSYLATED. CONSIST OF ABOUT 70% CARBOHYDRATE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA -!- TISSUE SPECIFICITY: EXPRESSED AND STORED EXCLUSIVELY IN MATURE INFECTIONS. PROTECTS THE EPITHELIA FROM EXTERNAL ENVIRONMENT. 01-ocr-1994 (REL. 30, LAST ANNOTATION UPDATE) INTEGUMENTARY MUCIN A.1 PRECURSOR (FIM-A.1) (PREPROSPASMOLYSIN) XENOPUS LAEVIS (AFRICAN CLAMED FROG). HAUSER F., GERTZEN E.M., HOFFMANN W.; EXP. CELL RES. 189:157-162(1990). -!- FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL. POTENTIAL.
INTEGUMENTARY MUCIN A.1.
P-TYPE 1.
P-TYPE 2.
14 X 9 AA TANDEM REPEATS.
7 X 4 AA REPEATS OF E-T-T-T.
P-TYPE 3. Score 206; DB 5; Length 400; Pred. No. 6.74e-13; -!- SIMILARITY: CONTAINS FOUR P-TYPE (TREFOIL) DOMAINS. REPEAT; SIGNAL; AMPHIBIAN SKIN; GLYCOPROTEIN BY SIMILARITY.
BY SIMILARITY. A 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE) 400 988391 CN; P-TYPE 4. -!- SUBCELLULAR LOCATION: SECRETED. BIOL. CHEM. 263:7686-7690(1988) Μ¥; 01-JUL-1989 (REL. 11, CREATED) MUCOUS GLANDS OF THE SKIN PROSITE; PS00025; P TREFOIL. 4.48; 42641 STANDARD; 20 400 63 1114 252 252 299 342 393 49 48 60 60 327 333 339 378 390 EMBL; M19971; M19971. AND 30% PROTEIN. PIR; A28172; A28172. HSSP; P01359; 1PCP. 400 AA; SEQUENCE FROM N.A. MEDLINE; 88227968. MEDLINE; 90316191 [2] CHARACTERIZATION 21 22 73 73 127 272 304 352 23 23 43 43 MEDLINE; 88227 HOFFMANN W.; MUA1 XENLA DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID CARBOHYD DISULFID DISULFID Query Match DISULFID DISULFID DISULFID SEQUENCE P10667; SIGNAL CHAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN SOURCE SO

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329 TEVVGTTPGQAPTAEPSGTTSVQVPTTEVISTAPVQMPTAE-STGMTPEKV-P-VSEVM 385 232 vvatkplaaaepvvvappatetpvvapaaasphvsvapavetavva-pvsasteppvaaa 290 386 GTILAEMSTPEATGMTPAEVSI-VVLSGTTAAQVTTTEWVETTARELPIPEP-EGPDASS 443 51 sspttsppttssspptsthtsspsststqssstaatsssapstassttsiptststettt 110 403 AEVSIVVLSGTTAAAQVTTTEMVETTARELPIPEPEGPDASSIMSTESITGSLGPLLDGTA 462 111 ttptastttpttttaapttaatttavttaastsaetttatat-atstptttttptsttttt 169 343 AEPSGITSVQVPITEVISTAPVQMPTAESTGMTPEKVPVSEVMGITLAEMSTPEATGMTP 402 231 VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE Gaps 172 vaapvaavpaavpvvapvlapavapavapvvaetpapppvaeipvatipecvaplipevs 1; Score 169; DB 8; Length 797; Pred. No. 8.77é-08; 64; Mismatches 84; Indels MEDLINE; 92295566.
TELFORD E.A.R., WATSON M.S., MCBRIDE K., DAVISON A.J.; VIROLOCY 189:304-316(1992).
EMBL, M86564, M86564.
PIR, 1886054, VGBEXI.
GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL. 71. EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1) 01-DEC-1992 (REL. 24, CREATED) 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE) 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE) GLYCOPROTEIN X. 797 AA. ż SER/THR-RICH. 797 AA; 80342 MW; 3610380 CN; 200 :: POTENTIAL. POTENTIAL. POTENTIAL. PRT; PRT; 291 tlttapetpalapvvaes 308 444 IMSTESITGSLGPLLDGT 461 Query Match 3.6%; Best Local Similarity 17.7%; Matches 32; Conservative GLYCOPROTEIN X PRECURSOR. STANDARD; STANDARD; 22 797 465 790 590

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-!- FUNCTION: RESPONSIBLE FOR EBV BINDING TO THE CR2 RECEPTOR ON HUMAN
                                             JIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE
                                                                                BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J., GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C., TUFFNELL P.S., BARRELL B.G.;
NATURE 310:207-211(1984).
                                                                                                                                     -!- SUBCELLULAR LOCATION: MOST ABUNDANT COMPONENT OF THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 169; DB 8; Length 907;
Pred. No. 8.77e-08;
                                    EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)
                                                                                                                                                                                 MEMBRANE; GLYCOPROTEIN; ANTIGEN; LATE PROTEIN.
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
ENVELOPE GLYCOPROTEIN GP340.
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EMBL; V01555, V01555.

PIR; A03762; QQBE21.

PIR; S33008; S33008.
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                                                                         MEDLINE; 84270667.
                                                                SEQUENCE FROM N.A.
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Matches

GLUCOSE RESIDUES SUCCESSIVELY FROM NON-REDUCING ENDS OF THE CHAINS 262 FGDSSGTLISRALWYTHTYLEPGPVTA-QVVLQAAIPLTSCGSS-PVPGTTDGHRPTAEA 319 481 ttsgaspytpspspwdngteskapdm-tsstspyttptpnatsptpayttptpnatsptp 539 320 PNTTAGQV-PTTEV-VGTTPGQAPTAEPSGTTSVQVPTTEVISTAP-VQMPTAESIGMTP 376 540 avttptpnatsptlgktsptsavttptpnatsptlgktsptsavttptpnatsptlgkts 599 421 fskapestttspt1nttgfadpntttg1pssthvptn1tapastgptvstadvtsptpag 480 BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A., GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JARGELS K., JONES M., LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V., WALGH S.V., WHITHERAD S., SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL 1,4-LINKED ALPHA-D-01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOPATION UPDATE)
GLUCOAMYLASE 51/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
STAI OR STA2 OR MAL5 OR YIR019C. -!- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES. PARDO J.M., IANEZ E., ZALACAIN M., CLAROS M.G., JIMENEZ A.; FEBS LETT. 239:179-184(1988). SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). EUKARYOTA, FUNGI, ASCOMYCOTINA, HEMIASCOMYCETES. PRT; 1367 AA. :: 600 ptsavttptpnatgptvgetspqanatnhtl 630 436 PEGPDASSI-MSTESITGSLGPLLDGTA-TL 464 SEQUENCE OF 1-242 AND 762-1331 FROM N.A. MEDLINE; 87194600. YAMASHITA I., NAKAMURA M., FUKUI S.; J. BACTERIOL. 169:2142-2149(1987). WITH RELEASE OF BETA-D-GLUCOSE. EMBL, M16165; M16165.
EMBL, X13857; X13857.
PIR, B26877; B26877.
PIR, A26877, A26877.
PIR, S4478; S48478.
LISTA, SCO1218; STAI.
SGD, LO002104; STAI.
PROSITE; PS00820; GLUCOAMYLASE. P08640; P08068; 01-AUG-1988 (REL. 08, CREATED) SEQUENCE OF 1-31 FROM N.A. STANDARD; EMBL; 247047; 247047. EMBL; M16164; M16164. STRAIN=S288C / AB972; MEDLINE; 89031230. SEQUENCE FROM N.A. STRAIN-SPX101-1C; LT 6 AMYH YEAST 임 임 g 쇰 ð δ δ δ

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HYDROLASE: GLYCOSIDASE: POLYSACCHARIDE DEGRADATION; GLYCOPROTEIN;	0000000000	
SIGNAL, MULICENE FAMILY.	qq	544
22 1367 22 1367 210 1367 vn 817 817	Qy	402
874 874 1367 AA; 136110 M	RES ID	RESULT ID MUC2
Query Match 3.6%; Score 167; DB 1; Length 1367;	DT	01-JU
39; I	TO TO	01-10
psssttesssap vptpsssttesssapaptpsssttesssap vts	8	MUC2
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634 -ssapvptpsssttesssapvptpsssttesssapvptpsssttesssapvtssttesss 692	S S	EOTHE [1]
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SFYS DICDI STANDARD; PKT; SUU AA. $P143\overline{2}8$ ;	& &	PETER
01-JAN-1990 (REL. 13, CREATED)	RI	J.
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) 01-FFR-1994 (REL. 28, LAST ANNOMATION UPDATE)	8 8	
COAT P	33	- <del>-</del>
COTA.	200	
EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;	88	
EUNYCETOZOA; DICTYOSTELIA.	8 5	- 1
SEQUENCE FROM N.A.	88	
STRAIN=AX4;	පු ස	LIMD
MEDILINE; YOUGHAS.	D¥0	EMBL
NUCLEIC ACIDS RES. 17:9489-9489(1989).	. DR	EMBL,
EMBL; X16491; X16491.	DR.	HSSP
PIK; 30/838; 30/838. DICTYDB: DD03007; COTA.	DR O	PROS]
SPORULATION; REPEAT.	KW	GLYCC
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rvative 64; Misma		REPER
424 gstedssalgsteessasgsaavssasgssaassspsssaassspsssaassspsssaa	LEI	REPER
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MEDLINE; 91358717.
TORIBARA N.W., GUM J.R., JR., CULHANE P.J., LAGACE R.E., HICKS J.W., PETERSEN G.W., KIM Y.S.;
PETERSEN G.W., KIM Y.S.;
PLIN: INVEST: 081405-1013(1991).
-!- FUNCTION: COATS THE EPITHELIA OF THE INTESTINES, AIRWAYS, AND OTHER MUCUS MEMBRANE-CONTAINING ORGANS.
-!- SUBCELLULAR LOCATION: SCRETEE:
-!- PTW: ALL CYSTEINE RESIDIES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISCURLE BONDS (BY SIMILARITY).
-!- PTW: ALL CYSTEINE BONDS (BY SIMILARITY). J.R. JR., HICKS J.W., TORIBARA N.W., ROTHE E.-M., LAGACE R.E., POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELES. ) SAPIENS (HUMAN). ARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; HERIA; PRIMATES. APPROXIMATE REPEATS. JUN-1994 (REL. 29, CREATED)
JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
IN 2 (INTESTINAL MUCIN 2) (FRAGMENTS). PRT; 2274 AA. ENCE OF 1-1270 AND 1291-2274 FROM N.A. BRONCHUS, CERVIX AND GALL BLADDER. IOL. CHEM. 267:21375-21383(1992) OPROTEIN; REPEAT; POLYMORPHISM. 4. 5. 6. 7A. 7A. 8A. 8B. 9B. 10A. 10B. ; P15445; 1PSH. ; 158370; 11TH EDITION. SITE; PS00022; EGF. STANDARD; SUBUNIT: MULTIMERIC. 791 791 807 823 839 846 853 869 908 947 947 947 3L; M74027; M74027. 3L; M94131; M94131. 3L; M94132; M94132. INE; 93016075. 792 808 808 824 840 854 870 870 909 932 948 972 UE=COLON; OR SMUC 8 HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Mismatches 90; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=SKIN;
MEDLINE; 93071556.
HAUSER F., HOFFMANN W.;
-3. BIOL, CHEM. 267:24620 (1992).
-!- FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 163; DB 5; Length 2274; Pred. No. 5.44e-07;
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T -> S (IN REF. 2).
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M -> T (IN REF. 2).
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01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
10-0CT-1994 (REL. 30, LAST ANNOTATION UPDATE)
INTECUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
XENOPUS LAEVIS (AFRICAN CLAMED FROG).
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TIONS, PROTECTS THE EPITHELIA FROM EXTERNAL ENVIRONMENT. LLULIAR LOCATION: SECRETED. EXTENSIVELY 0-GLYCOSYLATED.	TIESUE SPECIFICITI: SAIN. SIMILARITY: CONTAINS SIX P-TYPE (TREFOIL) DOMAINS. ALTERNATIVE PRODUCTION OF A NUMBER OF DIFFERENT FORMS OF THE PROTEIN		110	GINCOPROTEIN; ALTERNATIVE SPLICING.	8 X 8 AA APPROXIMATE TANDEM REPEATS,	/THR-RICH.	1-1. 1-2	1-3.	1-4.	1-5.	1-7.	œ [	P-IIPE 1. 8 X APPROXIMATE TANDEM REPEATS, THR-RICH		2-2.	2-3.	2-5.	2-6,	2-7.	2-8. P-TYPE 2.	3.	12 X APPROXIMATE TANDEM REPEATS,	1HK-K1CH.	3-2.	3-3.	3-4.	3~6.	3-7.	. 6-1. 6-1. 6-1.	3-10.	3-11.	3-12. D-MYDF A	P-IIPE 4. P-TYPE 5.	P-TYPE 6.	BY SIMILARITY.				BY SIMILARITY.		_	S	BY SIMILARITY.	
PROTECTS ' LOCATION: VELY O-GL	TISSUE SPECIFICITI SI SIMILARITY: CONTAINS : ALTERNATIVE PRODUCTS:	ED B1 A. 115. 55.	100	SKIN;	144	;	80 Y	104	112	128	136	144	301	224	239	249	275	287	294	301 347	394	522	411	419	431	443	4 60	472	4/9	498	515	77C	566 613	661	188	187	333	332	344	379	391	552	563 563	
IONS. P. LULAR L. XTENSIV	RITY: CATIVE PROPERTY	15, L02 5: A451	02; 1AT	AMPHIBIAN	81	;	18 81	97	105	121	129	137	218	218	225	240	260	276	288	30 e	353	402	402	412	420	432	454	461	473	492	499	516 525	572	620	162	182	307	317	327	364	374	526	546 546	;
INFEC SUBCE PTM:	1 ( )	MAI BE FRODUCED B EMBL; L02115; L02115. PIR: A45155; A45155.	HSSP; P040	REPEAT; AM	NON TER DOMAIN	;	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	DOMAIN	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT DOMAIN	DOMAIN	DOMAIN	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	NEPEAT DOM: IN	DOMAIN	DOMAIN	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	
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US-08-231-565A-27.rsp 13	BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. K -> E. C -> R. T -> A. MW; 2659094 CN;	<pre>Score 156; DB 5; Length 662; Pred. No. 4.41e-06; 24; Mismatches 61; Indels 1; Gaps 1;</pre>	<pre>stsqvaatktttpttttttttttttttttttttttttttttttt</pre>	454 tpt-tttkattttpttttttptttttkattttpttttttptttttkattttpttttttt 512 	T 10  T 11	
07:58	DISULFID 573 599 DISULFID 583 598 DISULFID 593 610 DISULFID 621 646 DISULFID 631 646 DISULFID 641 658 VARIANT 276 276 VARIANT 354 354 VARIANT 415 415 SEQUENCE 662 AA; 67774 MA;	Query Match 3.3%; Best Local Similarity 28.3%; Matches 34; Conservative	stsqvaatkttttpttttpt   ::   ::    GSSPVPGTTDGHRPTAEADNT	tpt-tttkattttpttttt 	VG50 HSV11 STANDARD; PRT; 670 AA. VG50 HSV11 STANDARD; PRT; 670 AA. 01-DEC-1992 (REL. 24, CAST SEQUENCE UPDATE) 01-DEC-1992 (REL. 24, LAST SEQUENCE CAPE SOURCE CA	
Aug 27 07 58	FT DIS FT DIS FT DIS FT DIS FT DIS FT VAR FT VAR FT VAR FT VAR	Query Match Best Local Matches	Db 394 Qy 302	Db 454 Qy 362	10	

## 01-APR-1990 (REL. 14, CREATED) 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE) 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE) 00THORN-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1). 0TEL OR OCT1. 6ALLUS GALLUS (CHICKEN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; 141 pstteseaapavtpddevkvpearvasaqtfsalsptq-spsefiaelarcaqpiaqand 199 266 SGTLISRALVVTH--TYLEPGPVTAQVVIQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTT 323 M.LYSODEIKTICUS. -!- CATALYTIC ACTIVITY: HYDROLYSES THE LINK BETWEEN N-ACETYLMURAMOYL RESIDUES AND L-AMINO ACID RESIDUES IN CERTAIN BACTERIAL CELL-WALL 383 -EVMGTILAEMSTPEATGMTP-AEVSIV-VLSGTTAAQVTTTEWVETTAR-ELPIPEPEG 438 27 sttlfssalivssygtpvallpvtaeateeqptn-aevaqapttetglvetpttettpgi 85 Gaps 4 X 67 AA APPROXIMATE TANDEM REPEATS. Query Match 3.2%; Score 148; DB 1; Length 671; Best Local Similarity 28.2%; Pred. No. 4.58e-05; Matches 55; Conservative 49; Mismatches 76; Indels 15; 01-0CT-1994 (REL. 30, CREATED) 01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE) 01-EEB-1995 (REL. 31, LAST ANNOTATION UPDATE) AUTOLYSIN (EC 3.5.1.28) (N-ACETYLAWRAMOYL-L-ALANINE AMIDASE). BUTENCOCOCCUS FARCALIS; (STREPTOCOCCUS FARCALIS). PROKARYOTA, FIRMICUTES; COCCI; STREPTOCOCCAEAE. [1] SEQUENCE FROM N.A. MEDLINE; 91358349. BELLYEAU C., POTVIN C., TRUDEL J., ASSELIN A., BELLEMARE G.; J. BACTERIOL. 173:5619-5623(1991). -!- FUNCTION: HYDROLYZES THE CELL WALL OF E.FAECALIS AND US-08-231-565A-27,rsp 739 AA. 70442 MW; 2419279 CN; PRT; HYDROLASE; CELL WALL; REPEAT. 200 lyas-vmmagaives 213 439 PDASSIMSTESITGS 453 STANDARD; 613 414 482 550 616 GLYCOPEPTIDES. EMBL; M58002; M58002. PIR; A38109; A38109. 671 AA; OCT1 CHICK P15143; Aug 27 07:58 REPEAT REPEAT REPEAT REPEAT SEQUENCE DOMAIN 임 δy g δ 염 염 ð ð

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[1] SEGUENCE FROM N.A. MEDLINE; 90138945. PETRYIAR B., STAUDT L.M., POSTEMA C.E., MCCORMACK W.T., THOMPSON C.B.;

DNA BIND SEQUENCE

Query Match Matches

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US-08-231-565A-27\_rsp

Aug 27 07:58

KLEAM J.D., ROULD M.A., AURORA R., HERR W., PABO C.O.;

LCELI 77:21-32(1994).

C -! FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR FOR SMALL NUCLEAR
RNA AND HISTORH H2B GENES.

-! SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
TO CLASS-2 POU.

RMIA AND JA31754; A33754.

RPIR, A31754; A33754.

RPIR, A31754; A33754.

RPIR, A31754; A37754.

RPIR, A91754; A37754.

RPIR, A91754; A37754. 578 qgaaqlpanaslaamaaaaglnpslmapsqfaaggal-lslnpgtlsgalspalmsnstl 636 459 slvattpslvtssaattltvspvlpltsaavtnlsvtgtsdttsnntatvistappassa 518 519 v-tspslspspasastseassasetsttqttstplssplgtsqvmvtasglqtaaaaal 577 393 STPEATCMIPAEVSIVVISGITAAQVITIEWVEITARELPI-PEP-EGPDASSIMSTESI 450 ASSA-MUNI N., MORTISHIRE-SMITH R.J., AURORA R., HERR W., WRIGHT P.E. PROSITE; PS00035; POU 1. PROSITE; PS00465; POU 2. HOMEOBOX; DNA-BINDING; TRANSCRIPTION REGULATION; ACTIVATOR; Query Match 3.2%; Score 149; DB 6; Length 743; Best Local Similarity 17.2%; Pred. No. 3.43e-05; Matches 33; Conservative 67; Mismatches 87; Indels VIRIDAE; DS-DNA ENVELOPED VIRUSES; LIPOTHRIXVIRIDAE X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 284-439. THERMOPROTEUS TENAX VIRUS 1 (STRAIN VT3) (TTV1) 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE) 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE) 474 AA. 379 438 HOMEOBOX. 743 AA; 76486 MW; 2873645 CN; POU DOMAIN. MEDLINE; 90245666. NEDMANN H., ZILLIG W.; NUCLEIC ACIDS RES. 18:2171-2171 (1990). EMBL; X14717; X14717. PRT; 01-NOV-1990 (REL. 16, CREATED) 01-NOV-1990 (REL. 16, LAST SEQ NUCLEAR PROTEIN; 3D-STRUCTURE TRANSFAC; T00640; -.
TRANSFAC; T00641; -.
MIM; 164175; 11TH EDITION.
PROSITE; PS00027; HOMEOBOX. STANDARD; ::::| |: 451 TGSLGPLLDGTA 462 637 a-tiqalasggs 647 CELL 73:193-205(1993) VIRAL PROTEIN TPX. SEQUENCE FROM N.A. MEDLINE; 90245666. VTP3\_TTV1V DNA BIND SEQUENCE P19275; 14 DOMAIN RRIAN REPRESENTATION OF THE PROPERTY OF THE PR g ð 셤 ð 원 ð g à PROC. NATL. ACAD. SCI. U.S.A. 87:1099-1103(1990). -!- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR FOR SMALL NUCLEAR 574 qgaaqlpanaslaamaaaaglnpglmassqfaaggal-lslnpgtlggalspalmsnstl 632 515 v-tspslspspsasasiseassasetsttqttstplssplgtsqvmvtasglqtaaaaal 573 393 STPEATGMTPAEVSIVVLSGTTAAQVTTTEMVETTARELPI-PEPEGPDASSIMSTESIT 451 455 slvattpslvtssaattltvnpvlpltspavtslsvtgttettsnntatvistappassa 514 -!- SUBCELLULAR LOCATION: NUCLEAR.
 -!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS, BELONGS 4; Gaps MEDLINE; 93241300. DEKKER N., COX M., BOELENS R., VERRIJZER C.P., VAN DER VLIET P.C., EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. HSSP; P14859; 10CT.
PROSITE; PS00027; HOMEOBOX.
PROSITE; PS000455; POU 1.
PROSITE; PS00465; POU 2.
HOMEOBOX; DNA-BINDING; TRANSCRIPTION REGULATION; ACTIVATOR; 3.2%; Score 149; DB 6; Length 739; 16.4%; Pred. No. 3.43e-05; 69; Mismatches 90; Indels 01-APR-1990 (REL. 14, CREATED) 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE) OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1). 743 AA. 739 AA; 75982 MW; 2865430 CN; POU DOMAIN. HOMEOBOX. PRT: RNA AND HISTONE H2B GENES STURM R.A., DAS G., HERR W.; GENES DEV. 2:1582-1599(1988) [2] STRUCTURE BY NMR OF 284-359. [3] STRUCTURE BY NMR OF 284-354, Best Local Similarity 16.4%; 32; Conservative KAPTEIN R.; NATURE 362:852-855(1993). 633 atiqal-assgslpi 646 452 GSLGPLLDGTATLRL 466 STANDARD; 348 TO CLASS-2 POU. EMBL; M29972; M29972. PIR; A34873; A34873. HOMO SAPIENS (HUMAN) NUCLEAR PROTEIN,
DOMAIN 278 SEQUENCE FROM N.A. MEDLINE; 89107993. MEDLINE; 93214991

OTF1 OR OCT1.

OCT1 HUMAN P14859;

5;

Gaps 5;

(1991). STROEMBERG K., STENMAN G., SAHLIN P., G.;	E SITE.  , O'CONNOR C.J.)  BAND VITAMIN AB.  AND COLIPASE FOIS.  S.  VATED BY BILE S.  ACYLGLYCEROL + 1  TERYL ESTER + H  MARY GLAND, AND  THE TYPE-B CARB  THE TYPE-B CARB  STERASE B 1.  STERASE B 1.  STERASE B 2.  LIPID DEGRADAT  SPLICING.  BILE-SALT-ACT  HEPARIN-BINDII	BY SIMILARITY.  MISSING (IN MINOR VARIANT).  16 X 11 AA TANDEM REPEATS, O-GLYCOSYLATED  17.  18.  19.  10.  11.
~ 50	THEN 13:030-640(1392):  THEN SEQUENCE, AND ACTIVE LINE; 9112282.  STIE D.L., CLEVERLY D.R.  STIE D.L., CLEVERLY D.R.  STIE D.L., CLEVERLY D.R.  TETT. 278:130-134(1991)  TETT. 278:130-134(1991)  TO DIETRRY TRICLYCERIDES  ENZYME REGULATION: ACTIVE GROUP.  CATALYTIC ACTIVITY: TRIA  TISSUE SPECIFICITY: MAMM SIMILARITY: BELONGS TO T.  "N MSACID. "M M M M M M M M M M M M M M M M M M M	569 668 668 668 668 679 679 679 679 679 679 679 679 679 679
FROM N. 9234785 9234785 J., NILS X S., BJ	IAL SEQUENCE, AND ACTION 15:000-040(159).  IAL SEQUENCE, AND ACTION 19:012282.  STIE D.L., CLEVERLY LETT. 278:190-194(1).  LETT. 278:190-194(1).  LETT. 278:190-194(1).  STIE D.L., CLEVERLY  LETT. 278:190-194(1).  OG DIETARY TRICINCINCINCINCINCINCINCINCINCINCINCINCIN	559 845 847 843 843 843 851 851 851 851 851 851 851 851 851 851
BIOCHEMISTRY 30:500-510 [4] SEQUENCE FROM N.A. MEDLINE; 92347858. LIDBERG U., NILSON J., ENERBAECK S., BURSELLI GENOMICS 13:630-640(199	SANCHICS   13:1030-040(1392)     PARTIAL SEQUENCE, AND ACTIVA   MEDLINE; 9112282.   CHRISTIE D.L., CLEVERLY D.R   CROWD. CREALITIC ACTIVITY: BENDING. TO CREMEL, MA94519, M94579.   CHRISTIE D.R. SANCH C.R. MANGARD STREEPENS. STATE CARBOXYLE PROSITE; PS00122; CARBOXYLE PROMAIN 21 142   DOMAIN 21 121 AND ACT SITE 214 214	ACT_SILE ACT_SILE DISULID DISULED DISULED CARBOHYD VARSPLIC DOMAIN REPEAT
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MEDLINE; 91006144. NILSSON J., BLAECKBERG L., CARLSSON P., ENERBAECK S., HERNELL O.,

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE

TISSUE=MAMMARY GLAND;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

HUI D.Y., KISSEL J.A.; FEBS LETT. 276:131-134(1990).

TISSUE=PANCREAS; MEDLINE; 91092399.

BJURSELL G.; EUR. J. BIOCHEM. 192:543-550(1990)

[3]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-MAMMARY GLAND;
MEDLINE; 91105134.
BABA T., DOWNS D., JACKSON K.W., TANG J., WANG C.-S.;

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6
                                                                                                                                                                                          276 VTHTYLEPGP-VT-AQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPT-TEV 332
                                                                                                                                                                                                                                333 VGTTPGQAPTAEPSGT-TSVQVPTTEVIST-APVQMPTAESTGM-TPEKVPVSEVMGTTL 389
                                                                                                                                                                                                                                                                      390 AEMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTES 449
                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (REL. 17, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-EB-1994 (REL. 28, LAST ANNOTATION UPDATE)
BILE-SALT-ACTIVATED LIPASE PRECURSOR (EC 3.1.1.3) (EC 3.1.1.13) (BAL)
(BILE-SALT-STHUGLATED LIPASE) (BSSL) (CARBOXYL ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) (PANCREATIC LYSOPHOLIPASE).
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                                                       3 THR-PRO REPEATS REGIONS AND TWO NEAR IDENTICAL REPEATS.
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EUTHERIA; PRIMATES.
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                                                                                                                                              Score 144; DB 9; Length 474;
Pred. No. 1.44e-04;
                                                                                                                                                                    36; Mismatches 90; Indels
US-08-231-565A-27 rsp
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                                                                                                                   167 THR-PRO(N).
49507 MW; 1624091 CN;
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Best Local Similarity 25.8%;
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                        PIR; S06686; S06686.
PIR; S15921; S15921.
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474 AA;
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Query Match 3.1%; Score 147; DB 1; Length 742; Best Local Similarity 24.6%; Pred. No. 6.11e-05; Matches 42; Conservative 50; Mismatches 67; Indels 12; Gaps 12;

FT REPEAT SQ SEQUENCE

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627 -pptgd-sgappvp-ptgds-gappvp-ptgds-g-appvpptgdagppvpptgdsgap 679 :||::||::|||:::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|

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Search completed: Tue Aug 27 08:10:37 1996 Job time: 61 secs.

Aug 27 18:55

and is derived by analysis of the total score distribution.

SUMMARIES

US-08-231-565A-27.rge

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

WPsrch\_tpn n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols

Tue Aug 27 18:46:19 1996; MasPar time 1302.69 Seconds 1156.982 Million cell updates/sec Run on:

Tabular output not generated.

Title:

Description: Perfect Score:

>US-08-231-565A-27 (1-661) from US08231565A.pep 7622

1 ATGGAYYTNGTNYTNAARMG.......1NYTWASNGGNCARCARGTN 1983 TACCTRRANCANRANTYKC........ N.A. Sequence:

TABLE bktranslate2 Gap 30 Scoring table:

Dbase 0; Query 0 Nmatch STD: 270440 seqs, 380027776 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

embl-new3 1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:VRT

16:VIR1 17:VIR2

genbank 92 Database:

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5 32:INV6 33:INV6 33:INV6 33:INV6 33:INV6 33:INV6 33:INV6 33:INV6 33:INV6 33:INV7 40:INV3 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7 46:PLN8 47:PLN 46:PLN8 53:RN17 56:PR18 56:PR18 56:PR18 56:PR19 56:PR110 57:PR11 58:PR115 57:PR15 57:PR15 56:PR113 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6

66:R0D7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3 73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

genbank-newl 80:ECT 81:INV1 82:INV2 83:WAM 84:PHG 85:PLN 86:PRI 87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT u-embl45 92

S73003 2130 bp mRNA PRI 25-JAN-1995 gp100=melanocyte lineage-specific antigen/Pmell7 homolog [human,

mRNA, 2130 nt].

DEFINITION ACCESSION KEYWORDS SOURCE

RESULT LOCUS

g639589 human.

NID

ALI GNMENTS

93:part1 Database:

Database

Mean 71.748; Variance 179.232; scale 0.400

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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	~ 5	CRHC1 BASACB	40 68 65	40 68 65
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Bacillus amyloliquefa pSacRII Pl cloning ve	. 5	0/1511100	65	65
Rat heat shock	Ę	RATHSP27A	66 86775	66 86775
hsp 27=heat shock pro		867755	3	3
Human voltage-gated p	S	HUMVENHK2	28	28
Pseudomonas aeru		PA47920	Π :	
Bovine bone mRNA for	_	BEBULAR	3 8	3 8
Lemur (ring-tailed)		LEMINVOL	28	28
Human mRNA.	æ	HUMU2AF1RA	98	98
Human mRNA	≴.	HSU2AF1RA	01 8	01 8
Methanobacterium	_	MT019363	ς:	?:
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Mus musculus		MM003560	1 13	1 13
		MURSPHB	62	62
Mus musculus	A1	MUSHSP25A1	62	62
Murine mRNA(pP25a)		MURSPH	62 MURSPH	62 MURSPH
	PS	MUSHSP25PS	62 MUSHSP25P	62 MUSHSP25P
Mus musculus	Æ	MUSHSP25A	62	62
Sorghum vulgare mRNA	;	SVPEPC	45	45
Herbaspirilium	٧.	HEUNIFABX	77	7
S.vurgate rero		SVFEFCAR	ה ח	C#

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by A.Vogel, 23-FEB-1990

IMSTESITGSLGPLIDGTATLALVKRQVPLDOVLYRYGSFSVTLDIVQGIESAEILQA VPSGEGDAFELIVSCQGGLPKEACMEISSPGCQPPAQRLCQPVLPSPACQLVLHQILK GGSGTYCLAVSLADTNSLAVVSTQLIMPGQEAGLGQVPLIVGILLVLMAVVLASLIYR RRLMKQDFSVPQLPHSSSHWLRLPASSALVPLVRIAPSSVGSRSEYSHMML" QLRTKAMNRQLYPEWTEAQRLDCWRGGQVSLKVSNDGPTLICANASFSIALNFPGSQK VLPDGQVIWVNNTIINGSQVWGGQPVYPQETDDACIFPDGGPCPSGSWSQKRSFVYVW KTWGQYWQVLGGPVSGLSIGTGRAMLGTHTMEVTVYHRRGSRSYVPLAHSSSAFTITD QVPFSVSVSQLRALDGGNKHFLRNQPLTFALQLHDPSGYLAEADLSYTWDFGDSSGTL ISRALVVTHTYLEPGPVTAGVVIGAAIPLTSCGSSPVPGTTDGHRPTAEAPNTTAGOV PTTEVVGTTPGQAPTAEPSGTTSVQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVM /db\_xref="PID:g386754" /translation="RGIRKNTMDLVLKRCLLHIAVIGALLAVGATKVPRNQDWLGVSR **GTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASS** NCBI 322 caggttatctgggtcaacaataccatcatcaatgggagccaggtgtgggaggacaggca 381 ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:| 142 accaaagcctggaacaggcagctgtatccagagtggacagaagcccagagacttgactgc 201 202 tggagaggtggtcaagtgtcctcaaggtcagtaatgatgggcctacactgattggtgca 261 441 caaqttctaqqqqqcccaqtqtctqqqqctqaqcattqqqacaqqqcaqqqqctqqqqc 561 381 81 9 Gaps /note="melanocyte-specific secreted glycoprotein; 22 atggatctggtgctaaaaagatgccttcttcatttggctgtgataggtgctttgctggct gtgtatccccaggaaactgacgatgcctgcatcttccctgatggtggaccttgcccatct ;; Length 2114; Indels 416; Mismatches 436; 96.2%; Score 7334; DB 55; 57.0%; Pred. No. 0.00e+00; /organism="Homo sapiens" 575 g Location/Qualifiers /codon start=1 586 c gi: 386754 Matches 1129, Conservative <1..2028 1..2114NCBI gi: 183559 Local Similarity ๙ 469 Query Match source BASE COUNT 181 262 241 322 382 442 421 502 CDS FEATURES Best ORIGIN 셤 õ g ð 원 δ g δ 임 δ g δ g δ 염 δ 염

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à	481		CARTTYYTNGGNGGNCCNGTNWSNGGNYTNWSNATHGGNACNGGNMGNGCNATGYTNGGN	540
Q	562			621
ð	541			009
g	622		gctcattccagctcagccttcaccattactgaccaggtgcctttctccgtgagcgtgtcc	681
δ	601			099
g	682		cagttgcgggccttggatggaggaacaagcacttcctgagaaatcagcctttgaccttt	741
ò	661			720
qq	742		gccctccagctccatgaccccagtggctatctggctgaagctgacctctcctacacctgg	801
δy	721			780
g Q	802		gactttggagacagtagtggaaccctgatctctcgggcacttgtggtcactcatacttac	861
δ	781			840
qq	862		ctggagcctggcccagtcactgccaggtggtcgtcctgcaggctgccattcctctcacctcc	921
δ	841			006
QQ	922		tgtggctcctccccagttccaggcaccacagatgggcacaggccaactgcagaggcccct	981
δλ	901			096
g	982		aacaccacagctggccaagtgcctactacagaagttgtgggtactacacctggtcaggcg	1041
٥y	961			1020
g	1042		ccaactgcagagcctctggaaccacatctgtgcaggtgccaaccactgaagtcataagc	1101
δò	1021			1080
g	1102		actgcacctgtgcagatgccaactgcagagagcacaggtatgacacctgagaaggtgcca	1161
δ	1081			1140
ą	1162		gtttcagaggtcatgggtaccacactggcagagatgtcaactccagaggctacaggtatg	1221
à	1141			1200
g	1222		acacctgcagaggtatcaattgtggtgctttctggaaccacagctgcacaggtaacaact	1281
δ	1201			1260
Op	1282		acagaqtggqtggagaccacagctagagatacctatccctgagcctgaaggtccagat	1341
à	1261			1320
qq	1342		gccagctcaatcatgtctacggaaagtattacaggttccctgggcccctgctggatggt	1401
ð	1321			1380
g	1402		acagccaccttaaggctggtgaagagacaagtcccctggattgtgttctgtatcgatat	1461
δ	1381	ACNGCNACNYTNMGNYTNGTNAARMG		1440
QQ	1462		<pre>ggttcctttccgtcaccctggacattgtccagggtattgaaagtgccgagatcctgcag    ::    ::       :     :               </pre>	1521

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δ	y 1441	GGNWSNTTYWSNGTNACNYTNGAYATHGTNCARGGNATHGARMSNGCNGARATHYTNCAR 1500
đ	b 1522	gctgtgccgtccggtgaggggatgcatttgagctgactgtgtcctgccaaggcgggctg 1581
٥y	y 1501	GCNGTNCCNWSNGGNGARGGNGAYGCNTTYGARYTNACNGTNWSNTGYCARGGNGGNYTN 1560
QQ	b 1582	cccaaggaagcctgcatggagatctcatcgccaggtgccagcccctgcccagcggtg 1641
δ	у 1561	CCNAARGARCCNTGYATGGARATHWSNWSNCCNGGNTGYCARCCNCCNGCNGARMGNYTN 1620
qq	b 1642	tgccagcctgtgctacccagcccagcctgccagctggttctgcaccagatactgaagggt 1701   :  :  :      :     ::         :  :     :    :  :
ρ	y 1621	TGYCARCCNGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCARATHYTNAARGGN 1680
ପ	b 1702	<pre>ggctcggggacatactgcctcaatgtgtctctggctgataccaacagcctggcagtggtc 1761    ::                                   </pre>
δλ	у 1681	GGNWSNGGNACNTAYTGYTNAAYGTNWSNYTNGCNGAYACNAAYWSNYTNGCNGTNGTN 1740
QO	b 1762	agcacccagcttatcatgcctggtcaagaagcaggccttgggcaggttccgctgatcgtg 1821 ::
Qy	y 1741	WSNACNCARYTNATHATGCCNGGNCARGARGCNGGNYTNGGNCARGTNCCNYTNATHGTN 1800
QO	b 1822	ggcatcttgctggtgttgatggttgttgttgcatctctgatatataggcgcagactt 1881
٥y	y 1801	GGNATHYTNYTNGTNYTNATGGCNGTNGTNYTNGCNWSNYTNATHTAYMGNMGNYMGNYTN 1860
qa	b 1882	atgaagcacqutctcccqtaccccaqttgccacatagcagcagtagtgctgcgtcta 1941
٥y	y 1861	ATGAARCARGAYTTYWSNGTNCCNCARYTNCCNCAYWSNWSNWSNCAYTGGYTNMGNYTN 1920
qq	b 1942	co-cgcatcttctgctcttgtcccattggtgagaatagcccctctcagtgggcagcag 2000
δ	y 1921	CCNMGNATHTTYTGYWSNTGYCCNATHGGNGARAAYWSNCCNYTNYTNWSNGGNCARCAR 1980
QQ Q	b 2001	gt 2002 
δλ	у 1981	GT 1982
32	RESULT	•
<b>걸 점</b>	LOCUS DEFINITION	HSU01874 2026 bp mRNA PRI 27-MAY-1994   Human me20m mRNA, complete cds.
Ä	ACCESSION NID	
Z .	KEYWORDS	
Š	SOURCE ORGANISM	human. Homo sapiens
		Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
R	REFERENCE AUTHORS	1 (bases 1 to 2023) Maresh, G.A., Marken, J.S., Neubauer, M., Aruffo, A., Hellstrom, I.,
	TITLE	Helistrom, K. and Marquardt, H. Cloning and expression of the gene for the Melanoma-Associated ME20
	JOURNAL	Antigen DNA Cell Biol. 13, 87-95 (1994) Andrete
RI	REFERENCE	9423103 2 (bases 1 to 2026)
	AUTHORS TITLE JOURNAL	Š
		ıtical Research Institute, 3005 1st Ave, Seattle,
೮ 🖺	COMMENT FEATURES	NCBI gi: 494939 Location/Qualifiers

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>1	481	CARTTYYTNGGNGGNCGNGTNWSNGGNYTNWSNATHGGNACNGGNMGNGCNATGYTNGGN	540
Д	547	acacacacatggaagtgactgtctaccatcgccggggatcccggagctatgtgcctctt	909
>	541	ACNCAYACNATGGARGTNACNGTNTAYCAYMGNMGNGGGNWSNMGNWSNTAYGTNCCNYTN	009
д	109	gctcattccagctcagcttcaccattactgaccaggtgcctttctccgtgagcgtgtcc	999
>	601	GCNCAYWSNWSNWSNGCNTTYACNATHACNGAYCARGTNCCNTTYWSNGTNWSNGTNWSN	099
Д	199	cagttgcgggccttggatggagggaacaactcctgagaaatcagcctctgaccttt	726
>-	661	CARYTHMGNGCNYTNGAYGGNGGNAAYAARCAYTTYYTNMGNAAYCARCCNYTNACNTTY	720
Q	727	geoetecagetecatgaceceagtggetatetggetgaagetgacetetectacaectgg	786
>-	721	GCNYTNCARYTNCAYGAYCONWSNGGNTAYYTNGCNGARGCNGAYYTNWSNTAYACNTGG	780
Q	787	gactttggagacagtagtggaaccctgatctctcgggcacttgtggtcactcatac	846
>-	781	GAYTTYGGNGAYWSWASNGGNACNYTNATHWSWAGNGCNYTNGTNGTNACNTAY	840
q	847	otggagcctggcccagtcactgccaggtggtcctgcagggctgccattcctctacctcc	906
>-	841	YINGARCCNGGNCCNGTNACNGCNCARGTNGTNTNCARGCNGCNATHCCNYTNACNWSN	900
Д	907	007 tgtggctcctccccagttccaggcaccacagatgggcacaggccaactgcagaggccct 966	996
>	901	TETECH TO THE TETE THE TH	096
Д	196	aacaccacagctggccaagtgcctactacagaagttgtgggtactacacctggtcaggcg	1026
>-	961	AAYACNACHGCNCGRCARGTNCCNACNACNGARGTNGGNACNACNACNCCNGGNCARGCN	1020
Ф	1027	ccaactgcagagcctctggaaccacatctgtgcaggtgccaaccactgaagtcataagc	1086
>	1021	CCNACNGCNGARCCNWSNGGNACNACNWSNGTNCARGTNCCNACNACNGARGTNATHWSN	1080
а:	1087	987 actgcacctgtgcagatgccaactgcagagagcacaggtatgacacctgagaaggtgcca 114	1146
ب ح	1101	ACNOCANCINCARAL GCCURACHOCANGRANONACA COGRAL GACALCA GALGARAGA INCCA	1206
Ω	114	gtttcagaggtcatgggtaccacctggcagagatgtcaactccagaggctacaggtatg	1770
>-	1141	GTNWSNGARGTNATGGGNACNACNYTNGCNGARATGWSNACNCCNGARGCNACNGGNATG	1200
Д	1207	acacctgcagaggtatcaattgtggtgctttctggaaccacagctgcacaggtaacaact	1266
>	1201	ACNCCNGCNGARGINMSNATHGINGINYINWSNGGNACNACNGCNGARGINACNACN	1260
а	1267	acagagtgggtggagaccacagctagagagctacctatccctgagcctgaaggtccagat	1326
>-	1261	ACNGARTGGGTINGARACNACNGCNMGNGARYTNCCNATHCCNGARCCNGARGGNCCNGAY	132(
Д	1327	gccagctcaatcatgtctacggaaagtattacaggttccctgggcccctgctggatggt	1386
>-	1321	GCN#SN#SN#TH#TG#SN#CNGR#SN#TH#CNGGN#SN#TH#GCNCCN#TN#THGENG	1380
۵	1387	cttaaggctggtgaagagacaagtccc	1446
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Db 1447	<pre>ggttccttttccgtcaccctggacattgtccagggtattgaaagtgccgagatcctgcag 1506    ::    ::       :     :               </pre>		
Qy 1441	GGNWSNTTYWSNCTNACNYTNGAYATHCTNCARGCNATHGARWSNGCNGARATHYTNCAR 1500		
Db 1507	gctgtgccgtccggtgagggatgcatttgagctgactgtgtcctgccaaggcgggctg 1566	mRNA	⋖
Qy 1501		CDS	
Db 1567	cccaaggaagctgcatggagatctcatcgccaggtgccagcccctgcccagcggctg 1626		
Qy 1561			
Db 1627	tgccagcctgtgctacccagcccagctgctgttctgcaccagatactgaaggt		
Qy 1621	TGYCARCCNGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCARATHYTNAARGGN 1680		
Db 1687	<pre>ggctcggggacatactgcctcaatgtgtctctggctgataccaacagcctggcagtggtc 1746    ::                                   </pre>		
Qy 1681	GGNWSNGGNACNTAYTGYYTNAAYGTNWSNYTNGCNGAYACNAAYWSNYTNGCNGTNGTN 1740		
Db 1747	agcacccagcttatcatgcctggtcaagaagcaggggccttgggcaggttccgctgatc 1806		
0y 1741			
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1867	cttatgaagcaagacttctccgtaccccagttgccacatagcagcagtcactggctgcgt 1926 :	Query Ma Best Loc Matches	<b>နာ</b> ဝို့ရွ
Qy 1858	YTNATGAARCARGAYTTYWSNGTNCCNCARYTNCCNCAYWSNWSNWSNCAYTGGYTNMGN 1917	Db 12	~
Db 1927	ctaccccgcatcttctgctcttgtcccattggtgagaatagcccctcctcagtgggcag 1986		
Qy 1918	YINCCNMGNATHTTYTGYWSNTGYCCNATHGGNGARAAYWSNCCNYTNYTNWSNGGNCAR 1977	Db 72	2
0b 1987	caggt 1991   :	0y 61	
Qy 1978	CARGT 1982	Db 132	2
RESULT		Qy 121	=
LOCUS DEFINITION		Db 192	~
ACCESSION NID	M7348 g190105	Qy 181	=
KEYWORDS SOURCE		Db 252	~
OKGANISM		Qy 241	-
REFERENCE	butherla, Finalces, Haplofilm; Cataffilm; Hominidae (bases 1 to 2131)	Db 312	~
AUTHORS	Kwon, B. S., Chintamaneni, C., Kozak, C.A., Copeland, N.G., Gilbert, D.J., Jenking, N., Barton, D., Francke, U., Kobayashi, Y. and Vin V.	Qy 301	
TITLE	Almohanocyte-specific gene, Pmel 17, maps near the silver coat	Db 372	~
TAMATION	COLOL LOCUS OH MOUSE CHILDMOSOME TO SHU IS IN S STUCKHILL REGION OH human chromosome can be seen that should eat it is no 1201 0000 0000 11001)	Qy 361	-
MEDLINE	F10C, Nall, Acad. 5C1, 0.5.6. 80 (EU), 7.20-725. (1991) 2011/22 VEDT 1. 100105	Db 432	2
FEATURES source		Oy 421	

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QQ	1512	gctgtgccgtccggtgagggatgcatttgagctgactgtgtcctgccaaggcgggctg 157l
٥y	1501	GCNCTNCCNWSNGGNGARGGNGAYGCNTTYGARYTNACNGTNWSNTGYCARGGNGGNYTN 1560
DP	1572	cccaaggaagcctgcatggagatctcatcgccaggtgccagcccctgcccagcggtg 1631
Qy	1561	CCNAARGARGCNIGYATGGARATHWSNWSNCCNGGNIGYCARCCNCCNGCNCARMGNYTN 1620
<b>q</b> 0	1632	tgccagcctgtgctacccagcccagcctgccagctggttctgcaccagatactgaaggt 1691
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qq	1692	ggctcggggacatactgcctcaatgtgtctctggctgataccaacagcctggcatggtc 1751
λō	1681	GGNWSNGGNACNTAYTGYYTNAAYGTNWSNYTNGCNGAYACNAAYWSNYTNGCNGTNGTN 1740
qq	1752	agcacccagcttatcatgcctgtgcctgggattcttctcacaggtcaagaagcaggcctt 1811
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QO	1812	gggcaggttcggctgatcgtggggatcttgctggtgttgatggctgtggtgtgcatct 1871
δy	1780	GENCARCHICCNYTHATHGTINGGNATHYTHYTHYTHYTHYTHYTHYTHYTHGTNYTHATGCCNGTNGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHGTNYTHAGGTNGTNYTHGTNGTNYTHGTNYTHGTNYTHGTNYTHGTNGTNYTHGTNGTNGTNYTHGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG
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DEF	DEFINITION	<pre>human melanocyte-specific (pmel 1/) gene, exons 2-3, cds.</pre>
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2722)
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                                       Ol-JAN-1996 (Rel. 46, Created)
Ol-JAN-1996 (Rel. 46, Last updated, Version 1)
Human melanocyte-specific (pmel 17) gene, exons 2-5, and complete
                                                                                                                                                                                                                                                                                                                            and Immunology, 635 Barnhill Drive, Indianapolis, IN 46202, USA
                                                                                                                        Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae
                                                                                                                                                                          Kwon B.S., Kim K., Heng H.H., Shi X.M., Tsui L., Lee Z.H., Youn B., Pickard R.T.; "Genomic organization and FISH mapping of human pmel 17, the
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                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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1317 ggaacaagcacttcctgagaaatcagcctctgacctttgcctccagctccatgacccas	δλ	:   623 CNATHAC	
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Bailin,T., Lee,S.-T. and Spritz,R.A.
Genomic organization and sequence of D12553E (Pmel 17), the human
homologue of the mouse silver (si) locus
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Henry Mall, University of Wisconsin, Madison, WI 53706, USA
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Vertebrata, Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1178)
Bailin, T., Lee, S.-T. and Spritz, R.A.
Genomic organization and sequence of D12S53E (Pmel 17), the human homologue of the mouse silver (si) locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 570; DB 10;
Pred. No. 9.74e-58;
                                                                                                                                                                                                                                                                                                                                                /chromosome="12"
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.5%;
Best Local Similarity 56.0%;
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                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-JUL-1995) Richard A. Spritz, Medical Genetics, 445
Henry Mall, University of Wisconsin, Madison, WI 53706, USA
NCBI gi: 1125058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 ttccttcccaggtggtcaagtgtccctcaaggtcagtaatgatgggcctacactgattgg 446
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                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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                                                                     Human melanocyte protein Pmel 17 gene, exons 2 and 3.
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Pred. No. 9.74e-58;
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23-DEC-1995 (Rel. 46, Last upd
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Best Local Similarity 56.0%;
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AFELTVSCQGGIPKEACMEISSPGCQPPAQRICQPVLPSPACQLVIHQIIKGGSGTYC
LNVSLADTNSLAVVSTQLIMPQQEAGLGQVPLIVGILLVLMAVVLASLIYRRILMKQD
FSVPQLPHSSSHWIRLPRIFCSCPIGENSPLLSCQQV"
231 c 373 g 276 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSQ.LRALDGGNKHFLRNQPLTFALQLHDPSGYLAEADLSYTWDFCDSSGTL.ISRALVV
THTYLEPGPVTAQVVLQAAIPLTSCGSSPVPGTTDGHRPTAEAPNTTAGQVPTTEVVG
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                                                                                                                                                                                                                                                                                      join (U31808:158. 232, U31807:128. 241, U31807:400..546, U31797:95..229, U31797:623..781, U31797:1030..1755, U31798:382..496, U31798:736..821, U31798:932..1135, U31798:1238..1327, 298..432)
Henry Mall, University of Wisconsin, Madison, WI 53706, USA
NCBI gi: 1125061
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/map="12q13-q14"
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373 g 298

BASE COUNT ORIGIN

0 46; Mismatches 33; Indels 0; Gaps Score 511; DB 86; Length 1178; Pred. No. 8.65e-49; Query Match 6.7%; Best Local Similarity 46.6%; Matches 69; Conservative

281 cttctcccaatatcaggcgcagacttatgaagcaagacttctccgtaccccagttgccac 340 염

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401 atagcccctcctcagtgggcagcaggt 428 쇰

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Search completed: Tue Aug 27 19:08:20 1996 Job time: 1321 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_tpn

n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols

Tue Aug 27 19:08:38 1996; MasPar time 162.64 Seconds 867.178 Million cell updates/sec

Run on:

(1-661) from US08231565A.pep >US-08-231-565A-27 Tabular output not generated. Description:

1 ATGGAYYTNGTNYTNAARMG......TNYTN#SNGGNCARCARGTN 1983 TACCTRRANCANRANTTYKC......ANRANSWNCCNGTYGTYCAN 7622 Perfect Score: N.A. Sequence:

COED:

TABLE bktranslate2 Scoring table:

Gap 30

91712 seqs, 35561689 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Post-processing: Minimum Match 0% Listing first 45 summaries

n-geneseq23 Database:

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17

Mean 54.833; Variance 254.949; scale 0.215

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Pred. No.	i	_	0.00e+00	3.52e-02	6.56e-02	7.46e-01	2.10e+00	3.24e+00
Description	MART-1 melanoma antig	Sequence encoding mel	Melanoma-specific imm	Human Natriuretic Pep	B.amyloliquefaciens s	Degenerate Alteromona	Sequence encoding imm	Clone P25b
ei Ei	T02716	096055	T03760	010572	010498	094335	T05466	Q03970
80 BB	11	16	11	~	7	11	16	~
Length	2112	2115	2131	1047	2351	1065	36	755
* Query re Match Length DB I	6.7	9.96	87.9	2.3	2.3	2.1	2.0	1.9
Score	7374	7364	6699	177	173	157	150	147
Result	-	7	m	4	c 5	9	7	œ

P-PSDB; R84854

US-08-231-565A-27.mg Aug 27 18:59

3.24e+00		6.08e+01	2.35e+01	3.09e+01	4.65e+01	4.65e+01	2.35e+01	•	2.35e+01	•	•	2.69e+01	2.69e+01	6.08e+01	6.08e+01	3.54e+01	3.54e+01	2.35e+01	3.54e+01	2.69e+01	1.18e+02	9.06e+01	1.03e+02	9.06e+01	1.18e+02	7.94e+01	6.95e+01	7.94e+01	6.95e+01	9.06e+01	9.06e+01	1.03e+02	9.06e+01	1.03e+02	6.95e+01	1.03e+02	
Clone P25a	Human Natriuretic Pep	Sequence of a synthet	Human prepro-parathor	Human brain Expressed	Generic coding sequen	Bovine aFGF synthetic	All possible variatio	HCV envelope region n	Partial cDNA encoding	MF-alpha-1-hPTH fusio	Sequence of MF-alpha-	Sequence of hepatitis	3' end of Hepatitis A	Rat MR22 serotonin re	Rice starch branching	Dihydroxyacetone-synt	Sequence of clone enc	6kB fragment contg. P	The iga gene, encodin	Attenuated hepatitis	-	Desulphatohirudin (I)	Sequence encoding new	pucnv-953 Norwalk vir	V.fischeri flavin red	Merozoite surface ant	Degenerate Alteromona	Sequence encoding Ag5	TK C	Plasmid pGPe for clon	Vector pGPe.	Sequence encoding amy	Norwalk virus genome	Polycystic kidney dis	Ryanodine receptor ge		
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1.9	1.9	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.6	•		1.6		1.6	1.6	1.6	1.6	1.6	
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ALIGNMENTS

tumour-associated antigen; immunogen; diagnosis; prognosis; prophylaxis; therapy; vaccine; ds. cDNA25; MART-1; melanoma antigen recognised by T-cells; gpl00 antigen derivative; melanoma; metastatic melanoma; Location/Qualifiers /\*tag= a /note= "cDNA25 melanoma antigen" WO9529193-A2. 20-APR-1996 (first entry) MART-1 melanoma antigen cDNA25. T02716 standard; cDNA; 2172 BP. (USSH ) US SEC DEPT HEALTH. Rosenberg SA; 38..2038 21-APR-1995; U05063. 22-APR-1994; US-231565. 05-APR-1995; US-417174. Kawakami Y, Roser WPI; 95-382963/49. 02-NOV-1995. Mammalian. Key RESULT 

ö Gaps ö 2172; Score 7374; DB 17; Length 2 Pred. No. 0.00e+00; 416; Mismatches 436; Indels 96.78; 57.08; Best Local Similarity 57.0%; Matches 1130; Conservative Match Query

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ö 261 TGGMGNGGNGARGARANYTNAARGTNWSNAAYGAYGANCONACNYTNATHGGNGCN 240 300 360 441 420 501 480 CARTTYYTNGGNGGNCCNGTNWSNGGNYTNWSNATHGGNACNGGNMGNGCNATGYTNGGN 540 909 999 cagttgcgggccttggatggaggaacaagcacttcctgagaaatcagcctctgaccttt 741 141 201 321 381 621 681 502 caagttetagggggcccagtgtetgggetgagcattgggacaggcagggcaatgetggge 561 81 9 Gaps in the detection of melanoma cells. Tumour infiltrating lymphocytes atggatctggtgctaaaaagatgccttcttcatttggctgtgataggtgctttgctggct 1 ATGGAYYTNGTNYTNAARMGNIGYYTNYTNCAYYTNGCNGTNATHGGNGCNYTNYTNGCN gtgggggctacaaaagtacccagaaaccaggactggcttggtgtctcaaggcaactcaga accaaagcctggaacaggcagctgtatccagagtggacagaagcccagagacttgactgc tggagaggtggtcaagtgtccctcaaggtcagtaatgatgggcctacactgattggtgca aatgcctccttctctattgccttgaacttccctggaagccaaaaggtattgccagatggg caggitalcigggicaacaataccaicaataggagccaggigigggaggacagcca gtgtatccccaggaaactgacgatgcctgcatcttccctgatggtggaccttgcccatct GGNWSNTGGWSNCARAARMGNWSNTTYGTNTAYGTNTGGAARACNTGGGGNCARTAYTGG acacacaccatggaagtgactgtctaccatcgccgggggatcccgggagctatgtgcctctt geteattecageteageetteaceattactgaceaggtgeetttetecgtgagegtgtee Immunogenic peptides derived from the melanoma associated antigen may be used in the production of vaccines. Nucleotide sequences the .. 0 = = = cultured ex vivo and returned to melanoma particles, and when <del>..</del> = P-PSDB, R78646. Melanoma associated antigen gpl00 - used in vaccines and for encoding the immunogenic peptides may be used as primers and Length 2115; capable of binding to the melanoma associated antigen can be radiolabelled, they may be used to identify tumour deposits. Matches 1129; Conservative 416; Mismatches 437; Indels --575 G; Score 7364; DB 16; Pred. No. 0.00e+00; = = = = = Claim 2; Page 19-22; 40pp; English. 469 A; 96.6%; detection of tumours Local Similarity 2115 BP; = = = Sequence Query Match 142 22 82 61 121 202 181 262 241 322 301 382 361 442 481 295 682 421 541 622 601 Best ] අු ð a q g g à g ð 셤 셤 염 g 셤 임 δ δ δ δ δ ð à δ

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y 661	ь 742 у 721	рь 802 Оу 781	b 862 y 841	b 922 4 901	b 982 y 961	b 1042 y 1021	b 1102 y 1081	b 1162 y 1141	b 1222 y 1201	b 1282 y 1261	b 1342 y 1321	b 1402 y 1381	b 1462 y 1441	b 1522 y 1501	Db 1582 Qy 1561	0b 1642
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Melanoma-specific immunogen comprises epitope(s) homologous with pMel.17 - are highly potent stimulators of HLA-A2+CTL's useful in adoptive immuno-therapy
Disclosure; Page 19-20; 148pp; English.
A melanoma-specific immunogen homologous with pMel-17 (t03760) comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the group R82098-R82194 capable of eliciting a CTL response. The epitopes R82098-R82108 are of particular interest. The immunogen can be used for 1; 1761 1881 2001 1621 TCYCARCCNGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCARATHYTNAARGGN 1680 Gaps cccgcatcttctgctcttgtcccattggtgagaatagccccctcctcagtgggcagcag partial protection in mammals against melanoma peptides which are homologous with pMel-17 are highly potent stimulators of HLA-A2+ CTLs in several cell lines and can be used in immunotherapy or Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy; cytotoxic T cell; lymphocyte; HIA-A2; ss. Engelhard VH, Hunt DF, Shabanowitz J, Slingluff CL; 87.9%; Score 6699; DB 17; Length 2131; 56.2%; Pred. No. 0.00e+00; vative 416; Mismatches 440; Indels 21; 491 T; incorporated into immunogenic conjugates as vaccines. Sequence 2131 BP; 474 A; 589 C; 577 G; Melanoma-specific immunogen, pMEL17. 29-APR-1994; US-234784. (UYVI-) UNIV VIRGINIA PATENT FOUND. Cox AL, Engelhard VH, Hunt DF, SI WPI; 95-302688/39. .r 3 T03760 standard; DNA; 2131 BP. 25-MAR-1996 (first entry) Best Local Similarity 56.2%; Matches 1125; Conservative 16-FEB-1994; US-197399. 16-FEB-1995; U01991 gt 2003 || GT 1982 Homo sapiens. WO9522561-A2. 24-AUG-1995. Query Match 1861 2002 1702 1822 1801 1882 1942 1981 ð g ð Op ð 염 ð g ð 쇰 ð a ò DATE DE LA PERSONA DE LA PERSO g à

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1900	1 TNATHTAYMGNMGNWGNYTNATGAARCARGAYTTYWSNGTNCCNCARYTNCCNCAYMSNW	4 (	8 8
1932	3 tgatatataggggagagttatgaagaagattctccgtaccccadttgccacatagca	187	В
1840	GNCARGINCCNYTNATHGINGGNATHYINYTNGINYINATGGCNGTNGINYTNACCNWSNY	178	ò
1872	3 ggcaggttcggctgatcgtgggcatcttgctggtgttgatggctgtgggtccttgcatctc	181	엄
1780		174	õ
1812	cacccagcttatcat	175	g
1741	2 GN#SNGGNACNTAYTGYTNAAYGTN#SNYTNGCNGAYACNAYWSNYTNGCNGTNGTN#	1683	Š
1752	agggacatactgcctcaatgtgtctctggctgataccaacagcctggcagtg	1693	g
1681	CARCCNGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCARATHYTNAARGGN	162	οy
1692	3 gocagoctgtgctacccagcccagcctgccagctggttctgcaccagatactgaagggtg	1633	qq
1621	I : I	156	δy
1632	cat	157.	요
1561	:  ::     :: YGARYTNACNGTNWS	1503	δy
1572	gccgtccggtgaggggatgcatttgagctgactgtgtcctgccaaggcgggctg	151	g
1501	:-     :-	144	δy
1512	cttttccgtcaccctggacattgtccagggtattgaaagtgccgagatcctgcag	145	g
1441	C ONGCNACNYTNMGNYTNGTNAARMGNCARGINCCNYTNGAYTGYGTNYTNTAYMGNTAYG	1387	ò
1452	. تد	1390	g
1381	:    :  NYTNGAYG	132	ò
1392	saatcatgtctacggaaagtattacaggttccctgggcccctgctggatg	1333	Db
1321	• >-	126	ý
1332	3 cagaqtgggtggagaccacagctagagagctacctatccctgaggctccagatg	127	Ω
1261	2 CNCCNGCNGARCTWASNATHGTNGTNYTWASNGGNACNACNGCNCARGTNACNACNA	120	δ
1272	3 cacetgoagagtatcaattgtggtgettetggaaccacagetgcacaggtaacaacta	121	QQ
1201	THE STREET STREE	114	δ
1212	cagaggtcatgggtaccacac	115	OP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for the produ. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=114,952). The protein (or variants) can be used in treatment of
                                                                                                    Human Natriuretic Peptide Receptor B.
NPRB; ANP; ENP; Kidney failure; heart failure; protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 T;
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                                                                                                                                                                                                                               note= "binds natriuretic peptides A, B and C]"
                                                                                                                             hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                         'note= "GC and protien kinase activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 C;
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1993 ccctcctcagtgggcagcaggt 2014
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1961 CNYTNYTNWSNGGNCARCARGT 1982
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Q10572 standard; DNA; 1047 BP.
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                                                                                                                                                                                                                                                      /label= transmembrane domain
Domain 479..1047
                                                                                                                                                                                                                    'label= extracellular domain
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                                                                                        09-APR-1991 (first entry)
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                                                                                                                                                                                                                                                                                                                                   /label= N-glycos site
Modified -site 161..163
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Modified -site 244..246
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Modified -site 277..279
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Modified -site 195..197
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                                                                                                                                                             Peptide 1..22
/label= signal sequence
Protein 12
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23-JUN-1989; US-370673.
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Modified -site 35..37
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N-PSDB; Q10324.
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                                                                                                                                        Homo sapiens.
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                                                Gaps
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Score 177; DB 2; Length 1047;
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                                              Conservative 127; Mismatches 234; Indels
                      Pred. No. 3.52e-02;
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(DUPO ) DU PONT DE NEMOURS CO.
  Query Match 2.3%;
Best Local Similarity 13.7%;
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WPI; 91-051337/07.
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Nucleotide sequences encoding the immunogenic peptides may be used as primers and probes in the detection of melanoma cells. Tumour infiltrating lymphocytes capable of binding to the melanoma associated antigen can be cultured ex vivo and returned to mparticles, and when radiolabelled, they may be used to ident (See R78639-45) may be used in the production of vaccines. 2.0%; 9 A; Figdor CG; detection of tumours Best Local Similarity WPI; 95-284790/38. cumour deposits. Sequence 36 BP; P-PSDB; R78642 Homo sapiens. EP-668350-A1. protein bind protein bind protein\_bind protein\_bind 33-AUG-1995 Adema GJ, æ Sequence Query Match Query Match /\*tag= T05466; \*tag= /\*tag= \*tag= \*tag= Matches 염 გ a g გ PR PR 음 염 g, ö 1832 attgaaaaaagtaatgaagccgctgatcacttcaaacacggtaactgatgaaatcgagcg 1891 By transfecting a host (e.g. E. coli) with the degenerate A. hanedai luciferase alpha- and beta-subunit genes Q94335/36, a recombinant luciferase can be produced. The luciferase can be applied as an Gapa screening and re-cloning steps, (using probes based on the sequence of B.subtilis SacB), all the plaques were found to hybridise to the probes. Clones 2A and 2C containing the putative scaB[BamP] gene digested with EcoRI in preparation for a Southern transfer. The same SacB[Bsu] probes were used in the Southern hybridisation and both hybridised only with a 1.5kb fragment. Sequence analysis of this fragment showed it to be the sacB[BamP] gene. The sucrose regulatory region can be incorporated into stable vectors to control expression of heterologous genes in transformed B.subtilis. sequences were converted to Bluescript to give plasmids pBE300 and pBE301, respectively. DNA was isolated from the plasmids and digested with FroRT in preserve. amyloliquefaciens lambda ZAP phage plaques. After three successive enzymatic label in various diagnostic and examination reagents etc., useful in high sensitivity detection methods.

Note: original sequence given in non-IUPAC degenerate code.

Sequence 1065 BP; 213 A; 94 C; 191 G; 146 T; hanedai - useful as an enzymatic label in diagnostic reagents, DNA encoding luciferase from fluorescent bacterium Alteromonas ; 0 The levansucrase-encoding sequence was isolated from Bacillus Degenerate Alteromonas hanedai luciferase alpha-subunit gene Luciferase; alpha-subunit; diagnostic; reagent; recombinant; 582 T; Score 173; DB 2; Length 2351; Pred. No. 6.56e-02; Sucrose regulatable expression vector which can replicate production; enzymatic label; examination; degenerate; ss. 23; Mismatches 45; Indels derived from non-Bacillus subtilis Bacillus species for 506 G; 524 C; expression in many bacterial species Location/Qualifiers Claim 1; Pages 5-7; 16pp; Japanese. 739 A; Example; Fig 3; 44pp; English 294335 standard; DNA; 1065 BP Query Match 2.3%; Best Local Similarity 35.8%; Matches 38; Conservative 17-APR-1996 (first entry) 08-FEB-1994; JP-035450. (CHCC ) CHISSO CORP. Alteromonas hanedai. 22-AUG-1995, 08-FEB-1994; 035450 2351 BP; See also Q10497-7. P-PSDB; R75210. P-PSDB; R10671 J07222590-A Sequence /\*tag=

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ö 1744 INWSNACNACNACNARNWSRTTNGTRTCNGCNARNWSNACRTTNARRCARTANGTNCCNW 1685 1684 SNCCNCCYTTNARDATYTGRTGNARNACNARYTGRCANGCNGGNWSNGGNARNACNGGYT 1625 1624 GRCANARNCKYTGNGCNGGNGGYTGRCANCCNGGNWSNWSDATYTCCATRCANGCYTCYT 1565 190 ggnmgnacnaaracnytncargtnggnacnatgggngtngtnytyccnacngcncayccn 249  $70\ {
m ttyathmgnytnggngtngcnwsngargarytnggnttygayacntaytggacnytngar}$ 130 caycayttyacngarttyggnytnacnggnaayytnttygtngcngcngcnaayytnytn 189 Gaps Immunogenic peptides derived from the melanoma associated antigen Melanoma; antigen; vaccine; immunogen; primer; probe; detection; Melanoma associated antigen gp100 - used in vaccines and for the Sequence encoding immunogenic peptide of melanoma antigen gp100. ; 0 Score 157; DB 17; Length 1065; Pred. No. 7.46e-01; 61; Mismatches 137; Indels US-08-231-565A-27 mg 1564 INGGNARNCCNCCYTGRCANWSNACNGTNARYTCRAANG 1526 250 gtnmgncarytngargaygtnytnytnytngaycaratg 288 T05466 standard; cDNA to mRNA; 36 BP Location/Qualifiers identification; tumour; gp100; ss. Claim 7; Page 27; 40pp; English. /product= Immunogenic peptide.
protein\_bind 1..33 9.68; 25-JAN-1996 (first entry) 21; Conservative 14-FEB-1995; 200348. 16-FEB-1994; EP-200337. 21-DEC-1994; EP-203709. 10.36 7..36 7..33 (ALKU ) AKZO NOBEL NV. Aug 27 18:59

returned to melanoma

used to identify

Score 150; DB 16; Length 36;

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New protein P25 prodn. - using P25 cDNA synthesised in vitro from ehrlich Complementary (c) DNA was transcribed from Ehrlich ascites tumour poly-A mRNA and subsequent hybridisation of this with oligonucleotide probes resulted in 2 clones of which one (P25a) comprised this sequence. This clone was altered at the translation start site by site-directed mutagenesis (at Nde I site). This was then used to transform host cells and the prod. is useful in eg medical research. See also Q03970. ô 107 agccgcctcttcgatcaagctttcggggtgccccggttgcccgatgagtggtcgcagtgg 166 Gaps 010572; 09-APR-1991 (first entry) Human Natriuretic Peptide Receptor B. NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase. ö Score 147; DB 1; Length 909; Pred. No. 3.24e+00; 16; Mismatches 23; Indels /note= "binds natriuretic peptides A, B and C]" /note= "GC and protien kinase activity Location/Qualifiers Disclosure; fig 1; 6pp; German. ascites tumour cell total mRNA Q10572 standard; DNA; 1047 BP. /label= transmembrane domain Jomain 479..1047 'label= extracellular domain 1.9%; Best Local Similarity 40.0%; cytoplasmic domain /label= N-glycos site Modified -site 777..279 /label= N-glycos site Modified -site 349..351 26; Conservative 456..456 /label= N-glycos site Modified -site 161..163 /label= N-glycos site Modified -site 244..246 Modified -site 195..197 /label= signal sequence 23..455 /label= N-glycos site Modified -site 35..37 Modified -site 24..26 'label= N-glycos\_site /label= mature NPBR 1912 YTNMG 1916 167 ttcag 171 Homo sapiens. Query Match Peptide Protein /label= Domain Domain Matches DAYCE THE STATE ST

Ehrlich ascites tumour; protein P25; ss.

Mus musculus

RESULT
1D 00
AC 00
DT 22
DE C1
KW EL
OS M EL
CS C1
CS

Q03969 standard; DNA; 909 BP.

1912 YTNMG 1916

229 ttcag 233

22-AUG-1989 (first entry)

003969;

Clone P25a

Location/Qualifiers

29..751

/\*tag= a /label=P25 protein DD-273071-A. 01-NOV-1989.

169 agccgcctcttcgatcaagctttcggggtgccccggttgcccgatgagtggtcgcagtgg 228

8 8 8

Sequence of a synthetic crystalline 'silk' gene based on protein fibroid of silk fibre produced by Bombyx mori moth larvae Structural protein; microbial silk production; ds. 1922 GGNARNCKNA-RCCARTGNWSNWSRTGNGGNARYTGNGGNACNWSRAARTCYTGYT 1864 1803 NCCNACDATNARNGGNACYTGNCCNARNCCNGCYTCYTGNCCNGGCATDATNARYTGNGT 1744 | ||: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: 525 gsnmtahgkynnnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnng 584 · 585 acndnnnncnvtnycnrgsnndnnnndsnnndwmnrysnnndnvkgmannhnsnnsshgs 644 345 anvnnntnnnggtrndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgd 404 405 nnnaahysganknnwwtgrnnnwvkgannsdnnncandnddnscdktnnstnanvangtg 464 52; Conservative 104; Mismatches 178; Indels 2; Gaps kinase activity. The DNA can be inserted into expression vectors for the prodm. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or wariants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English. The sequence was derived from the DNA encoding natriuretic peptide 465 ntnnmngvssnnnnrknmannknnasmnwrnrwnnnnngnsnryhkgagsrntnsnrgssy receptor B, NPRB, having guanyl cyclase (GC) activity and protein Natriuretic protein receptor B - for diagnosis and treatment of Query Match 1.9%; Score 144; DB 2; Length 1047; Best Local Similarity 15.5%; Pred. No. 5.00e+00; 51 T; 83 G; 645 nkssncvvdsrnvnkntd-ygnasnrstannddnna 679 15 C; Location/Qualifiers 1047 BP; 87 A; N81094 standard; DNA; 202 BP Chang M, Goeddel D, Lowe D; WPI; 91-036711/05. N81094; 29-OCT-1990 (first entry) /label= N-glycos site Modified -site 600..602 22-JUN-1990; U03586. 23-JUN-1989; US-370673. /label= N-glycos\_site (GETH ) GENENTECH INC N-PSDB; Q10324 also be prepd misc feature Bombyx mori. 10-JAN-1991 Sequence Matches RESULT N8 N8 AC N8 DT 29 DE SE OF KW St KW g გ 쇰 g a გ 셤 ŝ g გ 요 g

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Recombinant plasmids contg. DNA region and lac Z gene portion produce novel silk-like structural proteins similar to Bombyx
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Edwards RM, Light JA, Nicholson K;
WPI; 88-355406/50.
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Claim 7; Page 5; 17pp; English.

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ö Saccharomyces mating factor alpha-1 sequences and amino acid alterations ö constructed by synthesising 16 smaller oligos (PA9-PA24) between 22 and 1972 CHASNARNARNGGNWSRTTYTCNCCDATNGGRCANWSRCARAADATNCKNGGNARNCKNA 1913 Protein consists of 2-6 crystalline regions each contg. a specific 59 AA sequence repeated contiguously 4-8 times. The SQ in n81094 was 46 ggaagtggagcaggtgcaggttctggtgctggagctggatcaggtgcaggtgctggatca 105 Prodn. of human parathyroid hormone - by recombinant expression using 244 ccnmgnaaraargargayaaygtnytngtngarwsncaygaraarwsnytnggngargcn 303 Gaps Gaps A DNA consisting of the base sequence shown in n81094 in claimed. patent method facilitates prodn. of components of novel silk-like structural proteins with properties absent in natural silks. ; 0 .; 0 Disclosure; Fig.1; 36pp; English. All possible variations of the DNA sequence coding for human Length 348; Query Match 1.7%; Score 126; DB 1; Length 202; Best Local Similarity 28.2%; Pred. No. 6.08e+01; Matches 24; Conservative 25; Mismatches 36; Indels 1.7%; Score 133; DB 14; Length 348 9.9%; Pred. No. 2.35e+01; ative 36; Mismatches 46; Indels 40 T; 41 T; preproparathyroid hormone are given in 090320. 60 63 85 G; Parathormone; parathyroid hormone; PTH; ss. 28 C; 34 C; 1861 TNARNCKNCKNTADDATNARNWS 1837 106 ggagctggtgctggtagtggagcag 130 Alestrom P, Gautvik KM, Oyen TB; WPI; 95-206306/27. Q90320 standard; DNA; 348 BP. 74 A; 42 A; Query Match 1.7%; Best Local Similarity 9.9%; 9; Conservative 03-NOV-1995 (first entry) Human prepro-parathormone 15-JAN-1992; US-821478. 02-JUL-1993; US-087471. 22-OCT-1986; US-921684. 14-AUG-1989; US-393851. 08-SEP-1989; US-404970. 29 bases in length. 22-ocT-1986; 921684. (GAUT/) GAUTVIK K M. (ALES/) ALESTROM P. 348 BP; Homo sapiens 30-MAY-1995. Sequence Matches RESULT 88888888 유 g, 쇰 g g გ.

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16-MAR-1994 (first entry)

on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes 188 caggetgetggggatacaaaataceetttetttaceataggageaettgggtagaatatt 247 Example 4; Pagé 200-201; 500pp; English. The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers Gaps type, and for prepn. of antisense sequences, probes and constructs. transcription; mapping; locations; chromosomes; chromosomal; ss. Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes EST00574 has a "poor" coding probability as evaluated using the Jene transcription product; genetic markers; tagging; in vivo; ; coding-region prediction program CRM. See also 059041-061440. Sequence  $405~\mathrm{BP}_i$   $111~\mathrm{A}_i$   $77~\mathrm{C}_i$   $76~\mathrm{G}_i$   $140~\mathrm{T}_i$ Length 405; Score 131; DB 8; Length 405 Pred. No. 3.09e+01; 12; Mismatches 24; Indels Generic coding sequence for human preproinsulin. Human brain Expressed Sequence Tag EST00574. (USSH ) US DEPT HEALTH & HUMAN SERVICE. Location/Qualifiers Adams MD, Moreno RF, Venter CJ. Hormone; insulin; diabetes; ss. N10053 standard; DNA; 416 BP uvery Match
Best Local Similarity 44.6%;
Matches 29; Conservative 17-0CT-1992 (first entry) 12-FEB-1993; U01294. 12-FEB-1992; US-837195. 32..34 26..28 29..31 Leu" Leu" /\*tag= a /note= "encodes Leu" /note= "encodes Arg" WPI; 93-272882/34. /note= "encodes 'note= "encodes 248 tqcaq 252 479 GGCAR 483 Homo sapiens. Homo sapiens. W09316178-A 19-AUG-1993 υ v /\*tag= /\*tag= N10053; ungure insure \*tag= unsure /\*tag= ungure DE PRESENTATION OF THE PROPERTY OF THE PROPERT 임 δ g ð 

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254..256
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'note= "encodes Ser"

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1411 CYTGNCKYTTNACNARNCKNARNGTNGCNGTNCCRTCNARNARNGGNCCNARNWSNCCNG 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This coding sequence is a generic coding sequence which covers DNA sequences able to code for the human preproinsulin amino acid sequence. The features table indicates where Leu, Ser or Arg codons are intended. These 3 amino acids cannot readily be specified by a single generic codon, hence the need for clarification. For each of Leu, Arg and Ser the following pairs of codons are what was intended, respectively: YTR and CTY (= Leu), MGR and CGY (= Arg)
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See also N10052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1351 IDATNWSYTCNGTNWSCATDATNWSNWSNGCRTCNGGNCCYT 1310
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Pred. No. 4.65e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 33; 50pp; French.
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Best Local Similarity 6.2%;
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25-SEP-1995 (first entry)
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US5401832-A.
28-MAR-1995.
24-DEC-1984; 685923.
24-DEC-1984; US-685923.
311..313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant human acidic fibroblast growth factor - used to promote cell growth, to promote wound healing, for vascular grafts and blood vessel repair.

The grafts and blood vessel repair of precisions of the same of cell growth, to promote wound healing, for vascular grafts and blood vessel repair.

Shaclosure; Table 1; 25pp; English.

Colliquoucleotides were synthesized on the basis of the amino cell sequence of cattle acidic fibroblast growth factor (aFGF) and used to construct a synthetic gene (given in Q88233) that incorporates codons preferred by E. coll or mammalian cells, unique cloning sites, etc. The preferred sequence is given in C88234. The synthetic gene can be mutated to obtain a human aFGF continued and the synthetic gene for production of recombinant protein (R74647).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 aaygargartgyytnttyytngarmgnytngargaraaycaytayaayacntayathwsn 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Mismatches 102; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO INC.
Gimenez-Gallego G, Kelly LJ, Linemeyer DL, Thomas KA;
                                                                                                                                                04_JUN-1987; US-054991.
04_MAY-1988; US-190293.
08-FEB-1991; US-654397.
25-SEP-1991; US-765472.
25-SEP-1992; US-951365.
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P-PSDB; R74648.
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127:enEST2 128:enEST3 129:enEST4 130:enEST5 131:enEST6 132:enEST7 133:enEST8 134:enEST9 135:enEST10 136:enEST11

US-08-231-565A-27 rst

Mean 69.416; Variance 71.291; scale 0.974 Statistics Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Query		ŝ			
Score	Match		DB DB	11	Description	Pred. No.
1000	7 30	153	1	0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	00TC00 0
3	5·C7	179	577	- 4	Stalk.il homo sapi	0.0040
93	25.4	621	136	$\sim$	rl Homo sapi	9.0
1812	23.8	638	114	3736	rl Homo s	0.0
1812	23.8	638	136	362	rl Homo s	0.0
1510	19.8	546	136	462	.rl Homo s	0.00
1510		546	114	N28746	rl Homo s	0
1350		521	118	N40290	rl Homo	0
1350		521	131	HS290283	'.rl Homo	0
1297	17.0	416	89	R78477	rl Homo	0.00e+00
1006	13.2	306	83	T29726	Homo sa	,00e+
974		286		50	9a02.rl Homo	3.85e-302
◡		430	113	N23118	57c12.s1 Homo	6.28e
948		430	130	HS118284	sl Homo	ø
877	11.5	431	113	N23111	sl Homo	3.75e-
877		431	129	HS111256	sl Homo	۳,
292		909	130	HS123264	rl Homo	÷
292		909	114	N29123	l.rl Homo	ij
173		495	19	H51731	rl Homo s	27e-13
171		28	130	HS128259	l.sl Homo s	1.07e-1
171		28	113	N23128	s Homo s	ij
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140		288	83	T31913	EST40905 Homo sapiens	2.62e-05
138	•	306	93		uman STS WI-6432.	.15e-0
137		338	40	HSDHEKL23	. sapiens partial	1.17e-04
134	•	354	ç;	HSCI/HU61	. sapiens parti	
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	Score 1939 1939 1812 1812 1812 1812 1812 1350 1350 1350 1360 1371 171 171 171 171 171 171 171 171 17		25.4 25.4 25.4 25.3 25.3 25.3 25.3 25.3 25.3 25.3 25.3	Match Length  25.4  25.4  621  25.4  621  25.4  621  25.4  621  25.4  621  25.4  621  25.4  621  25.4  621  17.7	Aatch Length DB ID  25.4 621 114 N28728 25.4 621 114 N28728 23.8 638 114 N28728 13.8 638 114 N28728 19.8 546 114 N28746 17.7 521 118 N40290 17.7 521 118 N40290 17.7 521 118 N40290 17.7 521 111 N28747 13.2 306 83 729726 12.4 430 130 H511828 12.4 430 130 H511828 12.4 430 130 H511828 12.5 58 130 H512326 3.8 506 114 N23113 11.5 431 112 H51212 2.2 58 130 H512326 3.8 506 13 N23113 1.5 431 113 N23128 1.9 493 113 N24647 1.9 493 113 N24647 1.9 493 113 N24647 1.8 360 127 CEK087C 1.8 442 55 R36012 1.8 442 55 R36012 1.8 442 55 R36012 1.8 442 55 R36012 1.7 192 12 H51837 1.7 431 27 H8737 1.7 511 98 H55883 1.7 511 98 H55883	Match Length DB ID Description  25.4 621 134 N28728

.....TNYTNWSNGCNCARCARGTN 1983

1 ATGGAYYTNGTNYTNAARMG.......tnyTNWSNGGNCARCARGTN TACCTRRANCANRANTYKC......anranswncCnGTYGTYCAY

TABLE bktranslate2 Cap 30

Scoring table:

Comp:

Dbase 0; Query 0

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STD

Nmatch

(1-661) from USO8231565A.pep 7622

Perfect Score: N.A. Sequence:

Description:

Title:

>US-08-231-565A-27

Tabular output not generated.

Run on:

Tue Aug 27 19:11:52 1996; MasPar time 767.73 Seconds 917.837 Million cell updates/sec

n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols

MPsrch\_tpn

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

ALI GNMENTS

118:gneST10 119:gneST11 120:gneST12 121:gneST13 122:gneST14 123:gneST15 124:gneST3 125:eneST1

103:EST96 104:EST97 105:EST98 106:EST99 107:EST100 108:EST101 109:gnEST1 110:gnEST2 111:gnEST3 112:gnEST4 113:gnEST5 114:gnEST6 115:gnEST7 116:gnEST8 117:gnEST9

98:EST91 99:EST92 100:EST93 101:EST94 102:EST95

93:STS3 94:STS4 95:STS5 96:STS6 97:STS7

Database:

15:EST12 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST33 33:EST33 34:EST34 42:EST42 43:EST34 44:EST44 45:EST45 46:EST46 41:EST44 42:EST42 43:EST59 60:EST46 46:EST46 47:EST47 48:EST48 49:EST59 56:EST56 57:EST5 56:EST56 57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST66 63:EST67 64:EST76 46:EST76 77:EST77 78:EST77 78:EST77 74:EST77 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80 81:EST81 88:EST88 89:EST89 90:EST90 91:STS1 92:STS2

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14

509049 seqs, 177673129 bases x 2

Minimum Match Of Listing first 45 summaries

Post-processing:

Searched:

EST--STS

Database:

m

LOCUS DEFINITION		621 bp omo sapiens 3 A53668 gly	N28728 621 bp mRNA EST 04-JAN-1996 yx67a12.rl Homo sapiens cDNA clone 266782 5' similar to SP:PIR:A53668 A53668 glycoprotein gp100 precursor, melanocyte	EST 82 5' simi precursor	04-JAN-1996 lar to , melanocyte
ACCESSION NID	lineage - human ;. N28728 g1146964	nan ;·			
K+.YMOKUS					

KEYWORDS SOURCE ΕĪ

(ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. 1st strand RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B human clone=266782 primer=T7 library=Soares melanocyte 2NbHM

Homo sapiens

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

REFERENCE

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 1 (bases 1 to 621)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., AUTHORS

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995) TITLE JOURNAL

WashU-Merck EST Project Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Email: est@watson.wustl.edu High quality sequence stops: 398

Source: IMAGE Consortium, LINL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1146964

/organism="Homo sapiens" Location/Qualifiers 1..621 source FEATURES

/clone="266782" /note="human"

Ļ 145 173 g 170 c <1..>621 a 125 BASE COUNT mRNA

ORIGIN

8 others

Gaps 316; Conservative 135; Mismatches 138; Indels 5; Length 621; Score 1939; DB 114; Pred. No. 0.00e+00; 25.4**%**; 53.2**%**; Query Match Best Local Similarity Matches

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aaagtattacaggttccctgggccccctgctggatggtacagccaccttaaggctggtga 120 61

1 ctagagagetacetatecetgageetgaaggtecagatgecageteaateatgtetacgg 60

셤 ð 염

US-08-231-565A-27 rst Aug 27 19:12

1343 ARMSNATHACNGGNWSNYTNGGNCCNYTNYTNGAYGGNACNGCNACNYTNMGNYTNGTNA 1402 1642 CCNGCNTGYCARYTNGTNYTNCAYCARATHYTNAARGGNGGNWSNGGNACNTAYTGYYTN 1701 1702 AAYGTNWSNYTNGCNGAYACNAAYWSNYTNGCNGTNGTNWSNACNCARYTNATHATGCCN 1761 300 359 360 ccagcctgccagctggttctgcaccagatactgaagggtggctcgggggacatactgcctc 419 420 aatgtgtctctggctgataccaacagcctggcagtggtcagcaaccagcttatcatgcct 479 480 ggtcaagaagcaggccttggnaaggttccgctgatccgtgggcancttgctggtgttgat 539 181 acattgtccaggtnatntgaaagtgccgagatcctgcaggctgtgcgtnccggtgagggg 240 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project"; est@watson.wustl.edu High quality sequence stops: 398 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL 121 agagacaagtcccctggattgtgttctgtatcgatatggttccttttccgtcaccctgg gatgcatttgagctgactgtgtcctgccaaggcgggctgcccaaggaagcctgcatggag ateteategecagggtgecageceetgeceageggetgtge-ageetgtgetaceage School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: ; contact the IMAGE Consortium (info@image.llnl.gov) for further 1821 GCCNGTNGTNYTNGCNWSNYTNATHTAYMGNMGNMCNYTNATGAARCARGAYTT 1874 Contact: Wilson RK WashU-Merck EST Project Washington University = = = = 591 SP:PIR:A53668 A53668 glycoprotein gp100 precursor, melanocyte Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; 540 ggctgtgggcctttcatctctgntataggc-ca-acttatgaagcaaacttt 05-JAN-1996 (Rel. 46, Created) 05-JAN-1996 (Rel. 46, Last updated, Version 1) yx67al2.rl Homo sapiens CDNA clone 266782 5' similar to :: --------ВЪ. Location/Qualifiers 621 standard; RNA; EST; information. NCBI gi: 1146964 <del>..</del> --<del>..</del> --Homo sapiens (human) lineage - human ;. :: Unpublished LT 2 HS728262 1 - 621241 301 RESULT ID HS ð 셤 염 임 음 임 셤 셤 염 ð Š à δ δ ò δ δ

/organism="Homo sapiens"

source

/clone="266782" /note="human"

<1..>621

621

Sequence Query Match

RNA

FFFFFS

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5

Gaps

5 621;

Length Indels

DB 136;

BP; 125 A; 170 C; 173 G; 145 T; 8 other;

8

1 ctagagagctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacgg

316; Conservative 135; Mismatches 138; / Match 25.4%; Score 1939; DB 136 Local Similarity 53.2%; Pred. No. 0.00e+00;

Matches

g δ 쇰 ð g δ g ð 셤 ð 셤 ò 요 δ g ò g ð 임 8

121 agagacaagtoccoctggattgtgttctgtatcgatatggttccttttccgtcaccctgg 180 |::| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|

121

acattgtccaggtnaintgaaagtgccgagatcctgcaggctgtgcgtnccggtgagggg 240 

181

gatgeatttgagetgaetgteetgeeaaggegggetgeecaaggaageetgeatggag 300 

241

atctcatcgccagggtgccagcccctgcccagcggctgtgc-agcctgtgctacccagc 359

301

360

aaagtattacaggttccctggggccccctgctggatggtacagccaccttaaggctggtga 120

61

(Pharmacia), digested with Not I and cloned into the Not I and Eco double-stranded cDNA was size selected, ligated to Eco RI adapters foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. normal 5; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; clone is available royalty-free through LLNL; contact the 1403 ARMGNCARGINCCNYINGAYIGYGINYINIAYMGNIAYGGNWSNITYWSNGINACNYING 1462 IMAGE Consortium (info@image.llnl.gov) for further information. 120 agagacaagtccccctggattgtgttctgtatcgatatggttccttttccgtcaccctgg 180 181 acattgtccaggtnatttgaaagtgccgagatcctgcaggctgtgcgtnccggtgagggg 240 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 9 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Gaps RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.  ${\tt RNA}$  from 1 ctagagagctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacgg 61 aaagtattacaggttccctgggccccctgctggatggtacagccaccttaaggctggtga 241 gatgcatttgagctgactgtgtcctgccaaggcgggctgcccaaggaagcctgcatggag Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo = = :::= :: = :: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 5; Length 638; others Indels 2 114; 123; Mismatches 127; Washington University School of Medicine Score 1812; DB 11. Pred. No. 0.00e+00; 4 153 sapiens" High quality sequence stops: 368 Source: IMAGE Consortium, LLNL Location/Qualifiers ð Email: est@watson.wustl.edu The WashU-Merck EST Project 173 /organism="Homo /clone="266806" WashU-Merck EST Project /note="human 23.8%; 54.0%; 299; Conservative 1 (bases 1 to 638) U Contact: Wilson RK Unpublished (1995) Fax: 314 286 1810 <1..>638 Tel: 314 286 1800 169 NCBI gi: 1146972 Homo sapiens Best Local Similarity Wilson, R. 133 Albino. This Query Match source ORGANISM BASE COUNT TITLE JOURNAL Matches AUTHORS REFERENCE 121 FEATURES ORIGIN g 염 셤 g 8 셤 õ ð δ

human clone=266806 primer=T7 library=Soares melanocyte 2NbHM
vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. 1st strand

cDNA was primed with a Not I - oligo(dT) primer

N28736 638 bp mRNA EST 04-JAN-1996 yx67c12.rl Homo sapiens cDNA clone 266806 5' similar to SP:PIR:A53668 A53668 glycoprotein gpl00 precursor, melanocyte

638 bp

N28736

LOCUS DEFINITION

RESULT

lineage - human ;.

g1146972

N28736

ACCESSION KEYWORDS SOURCE

1762 GGNCARGARGCNGGNYTNGGNCARGTNCCNYTNATH-GTNGGNATHYTNYTNGTNYTNAT 1820

ggctgtgggcctttcatctctgntatataggc-ca-acttatgaagcaaacttt 591

540

ggtcaagaagcaggccttggnaaggttccgctgatccgtgggcancttgctggtgttgat 539

480

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420

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180

240

300

359

Aug 27 19:12

1701 NAAYGTNWSNYTNGCNGAYA-CNAAYWSNYTNGCNGTNGTNWSNACNCARYTNATHATGC 1759 caatgtgtctctggctgataacaacagcctggcagtggtcagcacccagcttatcatgc 479 480 ctggtcaagaacaaggccttggnaaggttccgctgatcgtggggcatcttgctggtgtta 539 61 aaagtattacaggttccctgggcccctgctggatggtacagccaccttaaggctggtga 120 301 atctcatcgccagggtgccagcccctgcccagcgggtgtgc-agcctgtgctacccagc agagacaagtcccctggattgtgttctgtatcgatatggttccttttccgtcaccctgg acattgtccaggtnatttgaaagtgccgagatcctgcaggctgtgcgtnccggtgagggg gatgcatttgagctgactgtgtcctgccaaggcgggctgcccaaggaagcctgcatggag ccagcctgccagctggttctgcaccagatactgaagggtggctcggggaacatactgcct 1 ctagagagctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacgg Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson 05-JAN-1996 (Rel. 46, Created)
05-JAN-1996 (Rel. 46, Last updated, Version 1)
yx67fil.rl Homo sapiens cDNA clone 266829 5' similar to
SP:PIR:A53668 A53668 A52668 glycoprotein gpl00 precursor, melanocyte theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., BP. standard; RNA; EST; 546 'The WashU-Merck EST Project"; 1819 ATGGCNGTNGTNYT 1832 540 atgnetgtggeett 553 Homo sapiens (human) lineage - human ;. Unpublished. LT 5 HS746262 1-546 1760 121 241 360 420 181 요 δ g ð 염 ð 셤 δ 셤 ð g ð 염 ò 쇰 ð 셤 ð අ ð 5; ||:|| ||:|| ||:|| || ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| || 1582 ATHWSNWSNCCNGGNTGYCARCCNCCNGCNCARMGNYTNTGYCARCCNGTNYTNCCNWSN 1641 ccagoctgccagctggttctgcaccagatactgaagggtggctcgggggaacatactgcct 419 caatgtgtctctggctgataacaaacagcctggcagtggtcagcacccagcttatcatgc 479 est@watson.wustl.edu High quality sequence stops: 368 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further Gaps revaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University 05-JAN-1996 (Rel. 46, Created)
05-JAN-1996 (Rel. 46, Last updated, Version 1)
yx67cl2.rl Homo sapiens cDNA clone 266806 5' similar to
SP:PIR:A53668 A53668 Glycoprotein gpl00 precursor, melanocyte Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Rolman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., 5. Length 638; Sukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; BP; 133 A; 169 C; 173 G; 153 T; 10 other;

В.

HS736264 standard; RNA; EST; 638

Homo sapiens (human)

1-638

lineage - human ;.

δ

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23.8%; Score 1812; DB 136; 54.0%; Pred. No. 0.00e+00;

/organism="Homo sapiens"

source

/clone="266806"

/note="human"

Location/Qualifiers

information. NCBI gi: 1146972

"The WashU-Merck EST Project";

Unpublished

299; Conservative 123; Mismatches 127;

Local Similarity

Matches

Query Match

Sequence 638

mRNA

419

O.

7 acagagtgggtggagaccacagctagagagctacctatcctgagcctgaaggtccagat 66 114 Query Match Best Local source ORGANISM BASE COUNT Matches JOURNAL 187 REFERENCE AUTHORS FEATURES COMMENT ORIGIN g 合 셤 염 ð ð ð 10; 1620 NTGYCARCCNGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCAR-ATHYTNAARG 1678 1261 ACNGARTGGGTNGARACNAGNGGNGARYTNCCNATHCCNGARCCNGARGGNCCNGAY 1320 1560 NCCNAARGARGCNTGYATGGARATHWSNWSNCCNGGNTGYCARCCNCCNGCNCARMGNYT 1619 ggctgtgcgtcccggtgagggggatgcatttgagctgactgtgtcctgccaaggcgggct 306 367 gtgc-agcctgtgctacccagcccagcctgccagctggttctgcaccaggatactgaagg 425 gocageteaateatgtetacggaaagtattacaggtteeetgggeceeetgetggatggt 126 acagccaccttaaggctggtgaagagacaagtcccctggattgtgttctgtatcgatat 186 ggttccttttccgtcaccctggacattgtccaggtnatntgaaagtgccgagatcctgca 246 7 acagagtgggtggagaccacagctagagagctacctatccctgagcctgaaggtccagat 66 yx67f11.r1 Homo sapiens cDNA clone 266829 5' similar to SP:PIR:A53668 A53668 glycoprotein gp100 precursor, melanocyte 04-JAN-1996 Gaps est@watson.wustl.edu High quality sequence stops: 377 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. NCBI gi: 1146982 human clone=266829 primer=T7 library=Soares melanocyte 2NbHM agttggtnaagcaacccactttatcatgnctgggncaagaaacaggnctttgnaaag 542 Indels 12; Length 546; BP; 114 A; 145 C; 158 G; 120 T; 9 other; Score 1510; DB 136; Pred. No. 0.00e+00; 290; Conservative 116; Mismatches 119; /organism="Homo sapiens" IIRNA Location/Qualifiers /clone="266829 /note="human" 546 bp 19.8%; 54.0%; .ineage - human ;. <1..>546 Best Local Similarity g1146982 EST. N28746 N28746 Sequence 546 Query Match 9 source DEFINITION 63 127 307 426 486 mRNA Matches 187 247 ACCESSION KEYWORDS SOURCE ge S

US-08-231-565A-27.rst

ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. 1st strand (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuteroscomia; Chordata; Vertebrata; Gnathoscomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 546) This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.linl.gov) for further information. Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., frevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and MO 63108 cDNA was primed with a Not I - oligo(dT) primer 4444 Forest Park Parkway, Box 8501, St. Louis, Washington University School of Medicine /organism="Homo sapiens" Email: est@watson.wustl.edu High quality sequence stops: 377 Source: IMAGE Consortium, LLNL Location/Qualifiers The WashU-Merck EST Project Unpublished (1995) WashU-Merck EST Project Contact: Wilson RK Tel: 314 286 1800 Fax: 314 286 1810 NCBI gi: 1146982 1..546 Homo sapiens Wilson, R. Albino.

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/clone="266829" /note="human"

Gaps Indels 12; Length 546; 114; 116; Mismatches 119; Score 1510; DB 114 Pred. No. 0.00e+00; 19.8%; 54.0%; 290; Conservative Similarity

9 others

ų 120

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158

145 c

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<1..>546

- 1261 ACNGARTGGGTINGARACNACNGCIMGNGARYTINCCINATHCCNGARCCNGARGGNCCNGAY 1320 67 gccagctcaatcatgtctacggaaagtattacaggttccctgggcccctgctggatggt 126
- 1381 ACNGCNACNYTNMGNYTNGTNAARMGNCARGTNCCNYTNGAYTGYGTNYTNTAYMGNTAY 1440 127 acagccaccttaaggctggtgaagagacaagtccccctggattgtgttctgtatcgatat 186
- ggttccttttccgtcaccctggacattgtccaggtnatntgaaagtgccgagatcctgca
- ð

vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B

RESULT LOCUS

NID

 $\blacksquare$ 

Aug 27 19:12

IMAGE Consortium (info@image.llnl.gov) for further information

sapiens" Location/Qualifiers /organism="Homo NCBI gi: 1163835 1..521 FEATURES

/clone="268044" /note="human"

307 geceaaggaageetgeatggagateteategecagggtgecageceetgeecagegget 366

1500 RGCNGTNCCNWSNGGNGARGGNGAYGCNTTYGARYTNACNGTNWSNTGYCARGGNGGNYT 1559

247 ggctgtgcgtcccggtgagggatgcatttgagctgactgtgtcctgccaggcgggct 306 :|| || | | : || || :|| || :| || :|

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1620 NTGYCARCCNGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCAR-ATHYTNAARG 1678

367 gtgc-agcctgtgctacccagcccagcctgccagctggttctgcaccaggatactgaagg 425

486 aqttqqtnaaqcaacccactttatcatqnctqqqncaaqaaacagqnctttqnaaaq 542

426

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others ىد 110 6 135 150 c æ 122 BASE COUNT

Length 521; Score 1350; DB 118; Pred. No. 0.00e+00, 17.78; 58.88; Local Similarity Query Match ORIGIN

4; 9 Gaps 1 atgaccctagtggctatctggctgaagctgacctctcctacacctgggactttggagaca 4; Indels 65; Mismatches 100; 241; Conservative Matches අ

61 gtagtggaaccetgatetetegggeaettgtggteacteataettaeetggageetggee 120 g ð

à

cagicacigcccaggiggtectgcaggeigecaticcicicacciccigiggciccicc 180 121 셤 δ

240 181 cagttccaggcaccacagatgggcacaggccaactgcagaggcccctaacaccacagctg g

Š

300 241 geceasgigectactacagaagitigiggiactacacciggicaggegecaacigeagage g

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P.

RI sites of a modified pT7T3 vector (Pharmacia). Library

yx80c07.rl Homo sapiens cDNA clone 268044 5' similar to PIR:A53668 A53668 glycoprotein gp100 precursor, melanocyte lineage - human ;. N40290

22-JAN-1996

EST

**IIRNA** 

521 bp

N40290

RESULT LOCUS DEFINITION

ACCESSION

KEYWORDS SOURCE

NID

q1163835

974 GNCARGTNCCNACNACNGARGTNGTNGGNACNACNGGNCARGCNCCNACNACNGCNGARC 1033 ò

301 cctctggaaccacatctgtgcaggtgccaaccactgaagtcataagcactgcacctgtgc 360 쇰

δ

361 agaatgcccaactgcagagagcacaggtatggacacctggagaaggtgcc 410 g

ð

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Homo sapiens

ORGANISM

Albino.

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo

REFERENCE AUTHORS

1 (bases 1 to 521)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

The WashU-Merck EST Project

Wilson, R.

Unpublished (1995)

TITLE JOURNAL

COMMENT

standard; RNA; EST; 521 LT 8 HS290283 N40290; RESULT.
11D HS
AC N4
AC N4
AC N4
AC N4
AC N4
AC N6
AC

26-JAN-1996 (Rel. 46, Created) 26-JAN-1996 (Rel. 46, Last updated, Version 1) yx80c07.r1 Homo sapiens cDNA clone 268044 5' similar to PIR:A53668 A53668 glycoprotein gp100 precursor, melanocyte lineage - human ;.

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Homo sapiens (human)

1 - 521

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hohman M., Hutman M., Kucaba T., Le M., Iennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Materston R., Williamson A., Wohldmann P., Wilson The HashU-Merck EST Project";

Unpublished

Email: est@watson.wustl.edu High quality sequence stops: 340 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Washington University School of Medicine

WashU-Merck EST Project

Contact: Wilson RK

US-08-231-565A-27 rst

9 Deuterostomia, Chordata, Vertebrata; Gnathostomata, Osteichthyes; Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria; vector. Library went through one round of normalization. Library This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand 1289 ARYTNCCNATHCCNGARCCNGARGGNCCNGAYGCNWSNWSNATHATGRSNACNGARWSNA 1348 aagteeecetggattgtgttetgtategatatggtteetttteegteaeectgggacatt 180 gtccagginatttgaaagigccgagaiccigcaggcigigcgitccggigaggggaigc 240 61 ttacaggttccctgggccccctgctggatggtacagccaccttaaggctggtgaagagac 120 241 atttgagctgactgtgcctgccaaggcgggctgcccaaggaagcctgcatgggagatct 300 301 categocagggtgccagcccetgcccagcngctgtgccagcctgtgcttacccagccca 360 9 Gaps 1 (bases 1 to 416)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and 1 agctacctatccctgagcctgaaggtccagatgccagctcaatcatgtctacggaaagta Eutheria; Archonta; Primates; Catarrhini, Hominidae; Homo. 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 9 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 416; 3 others 95; Mismatches 92; Indels constructed by Bento Soares and M.Fatima Bonaldo. :89 Washington University School of Medicine Possible reversed clone: polyT not found. Score 1297; DB 68, Pred. No. 0.00e+00, 103 t /organism="Homo sapiens" High quality sequence stops: 320 Source: IMAGE Consortium, LLNL Location/Qualifiers ь Email: est@watson.wustl.edu The WashU-Merck EST Project Unpublished (1995) 119 /clone="144875" Contact: Wilson RK WashU-Merck EST Project /note="human Query Match 17.0%; Best Local Similarity 53.6%; 113 c 223; Conservative Fax: 314 286 1810 Tel: 314 286 1800 1..416 NCBI gi: 854770 Homo sapiens æ Wilson, R. 78 source ORGANISM BASE COUNT Matches 181 121 AUTHORS REFERENCE FEATURES ORIGIN 염 쉱 ŏ 임 쇰 à g g δ Š õ

With a Not I - oligo(dT) primer [5' AACTGGAGAATTGCGGGGAGAATTTTTTTTTTTTTTT 3'], double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773

(Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsitel=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed

human clone=144875 library=Soares placenta Nb2HP vector=pT7T3D

q854770

N. 1841 1 416 bp mRNA EST. 09-JUN-1995 yi73d06.rl Homo sapiens cDNA clone 144875 3' similar to SP:A41234 A41234 WELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ;.

LOCUS DEFINITION ACCESSION KEYWORDS SOURCE

7	Aug 27 19 12	H12 US-08-231-565A-27 rst
ខ្លួ	Contac School	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
ဥ္ပ	MO 631	MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
38	Consol	ree through
ဥ န	; cont	; contact the IMAGE Consortium (info@image.llnl.gov) for further
3 €	Key	watton. Not yr. 1100000 Location/Qualifiers
<b>Æ</b> 8		
	sonrce	5 L.C.L e
· E		
E. 1	į	/note="human"
- g	mkna Sequence	<1>>21 No. 122 A; 150 C; 135 G; 110 T; 4 other;
õ	Query Match	cch 17.7%; Score 1350; DB 131; Length 521;
B. B.	Best Local Matches 2	Similarity 58.8%; (41, Conservative
ą	-	stgaccctagtggctatctggctgaagctgacctctcctacacctgggactttggagaca 60
ā	734 P	:  :   ::      ::       :     :     :     :
ą	61 0	ataqtaqaaccctqatctctcqqqcacttqtqqtcactcatacttacctqqaqcctqqcc 120
à	794	SNWSNGGNACNYTNATHWSNMGNGCNYTNGTNGTNACNCAYACNTAYYTNGARCCNGGNC 853
g	121	ragicacigoccaggigitetigeaggeigeaticeteteaectectytygetectee 180
2	854 (	
ج	181	anti ceaggacacacaga nggasaggicaact gagaggicit aagacgaggig 240
3		
⋩	914	ZNGTNCCNGGNACNACNGAYGGNCAYMGNCCNACNGCNGARGCNCCNAAYACNACNGCNG 973
ą	241 9	gccaagtgcctactacagaagttgtgggtactacacctggtcagggggcaactgcagagc 300
⋩	974 G	GNCARGINCCNACNACNGARGINGTNGGNACNACNGCNCGNCGNCCNACNACNGARC 1033
ą	301 c	sctctggaaccacatctgtgcaggtgccaaccactgaagtcataagcactgcacctgtgc 360
\$	1034 0	::             ::
ą	361 a	agaatgcccaactgcagaggacacaggtatggacacctggagaaggtgcc 410
æ	1094 A	:                    ::

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1586 SIMSINCCNGGNTGYCARCCNCCNGCNCARMGNYTNTGYCARCCNGTNYTN-CCNWSNCCN 1644 ð

361 gccttgncagttggtttttgcaccagatacttaagggttggttggggacatattgc 416 = = = = 셤

1645 CCNT-GYCARYTNGTNYTN-CAYCARATHYTNAARGGNGGNWSNGGNACNTAYTGY 1698 ð

DEPINITION EST92123 Homo sapiens CDNA 5' end similar to melanocyte-specific protein Pmel 17 (GB:M77348) (HT:1391). 06-SEP-1995 RNA 306 bp 10

q611824 ACCESSION

KEYWORDS

human primer=M13 Reverse library=Human Skin. SOURCE

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Homo sapiens ORGANISM

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo

1 (bases 1 to 306) REFERENCE AUTHORS

Adams M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Sandek, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Gruber, J., Hudson, P., Klm, A., Kozak, D.L., Kunsch, C., Ji, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,

Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence TITLE

Unpublished (1995) Other\_ESTs: THC20616 JOURNAL COMMENT

The Institute for Genomic Research Contact: Venter, JC

932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056

Fax: 3018699423

information related to this EST, please contact the TIGR Database For clone availability, additional sequence and expression Email: tdbinfo@tdb.tigr.org (tdbinfo@tdb.tigr.org).

Location/Qualifiers 1..306 NCBI gi: FEATURES

/organism="Homo sapiens" /note="human" <1..>306 source RNA

75 t 6 98 77 c ø 63 BASE COUNT

ORIGIN

5 others

Length 306; Score 1006; DB 83; Pred. No. 0.00e+00; 13.2%; 54.4%; Best Local Similarity Query Match

US-08-231-565A-27.rst Aug 27 19:12

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; Gaps Indels 65; Mismatches :89 Conservative 161; Matches

9 1 qnqaqctacctatccctqaqcctqaaqqtccanatgccaqctcaatcatgtctacggaaa \_ :: \_ :: \_ :: \_ :: g

1286 GNGARYTNCCNATHCCNGARCCNGARGGNCCNGAYGCNWSNWSNATHATGWSNACNGARW 1345

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121 gacaagtcccctggattgtnttctgtatcgatatggttccttttccgtnaccctggaca 180 ð 쇰

ttgtccaggtgattgaaagtnccgagatcctgcaggctgtgccgtccggtgaggggatg 240 181

쇰 δ

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296 catttgagcttgactgtgtcctgccaaggcgggctgcccaaggaaagcctgcatgg 241 음 1526 CNTTYGARYIN-ACNGTNWSNTGYCARGGNGGNYINCCNAARGAR-GCNTGYATGG 1579 δ

IIRNA 286 bp R01509 11 RESULT LOCUS

ye79a02.r1 Homo sapiens cDNA clone 123914 5' similar to SP:A41234 A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ; 31-MAR-1995 DEFINITION

g751245 ACCESSION

R01509

KEYWORDS

SOURCE

I and cloned into the Pac I and Eco RI sites of the modified pT/T3

vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo

ORGANISM

REFERENCE

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens

AUTHORS

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 1 (bases 1 to 286) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

The WashU-Merck EST Project Unpublished (1995) Wilson, R. TITLE JOURNAL

Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Contact: Wilson RK WashU-Merck EST Project Tel: 314 286 1800

High quality sequence starts: 1 Email: est@watson.wustl.edu Fax: 314 286 1810

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality Possible reversed clone: similarity on wrong strand.

Location/Qualifiers 1..286 751245 NCBI gi: FEATURES

/organism="Homo sapiens" /clone="123914" /note="human"

4 others ų 59 b 81 86 c ๗ 20 BASE COUNT ORIGIN

ö Gaps ö Length 286; Indels 67; Mismatches 70; Score 974; DB 46; Pred. No. 3.85e-302; 51.8%; 147; Conservative Best Local Similarity Query Match Matches

1449 YWSNGTNACNYTNGAYATHGTNCARGGNATHGARWSNGCNGARATHYTNCARGCNGTNCC 1508 9 1 ttccgtcaccctggacattgtcngggaatttgaaagtgccgagatcctgcaggctgtgcc 셤 ð

셤

61 incccgigaggaggatgcatitgagcigacigitcigccaangcgggcigccaagga  $120\,$ 

ò

121 agectgeatggagateteategeeagggtgeeagceeetgeeeageggetgtgeageet 180 g ð

ggtgctanccagcccagcctgccagctggttctgcaccagatactgaagggtggctcggg 240 181 셤

1629 NGTNYTNCCNWSNCCNGCNTGYCARYTNGTNYTNCAYCARATHYTNAARGGNGGNWSNGC 1688 ð

241 gacatactgcctcaatgtgtctctggctgataccaacagcctgg 284 g

1689 NACHTAYTGYYTNAAYGTNWSNYTNGCNGAYACNAAYWSNYTNG 1732 ð

N23118 12 RESULT LOCUS

yx67c12.s1 Homo sapiens cDNA clone 266806 3' similar to SP:A41234 A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR 430 bp DEFINITION

28-DEC-1995

g1137268 N23118 ACCESSION

KEYWORDS SOURCE

human clone=266806 primer=m13 -40 forward library=Soares melanocyte (Pharmacia), digested with Not I and cloned into the Not I and Eco host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Homo sapiens ORGANISM

Deuterostomia, Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii, Choanata; Tetrapoda; Amniota; Mammalia; Theria; 1 (bases 1 to 430)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo REFERENCE AUTHORS

US-08-231-565A-27.rst Aug 27 19:12 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. Wilson, R.

The WashU-Merck EST Project TITLE JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK WashU-Merck EST Project

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine

Email: est@watson.wustl.edu Fax: 314 286 1810 Tel: 314 286 1800

High quality sequence stops: 288 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.linl.gov) for further information.

Location/Qualifiers NCBI gi: 1137268 FEATURES

/organism="Homo sapiens" 1..430

source

/clone="266806" /note="human" <1..>430

1 others 93 ð 115 107 cBASE COUNT

Length 430; Score 948; DB 113; Pred. No. 6.28e-292; 12.4%; 53.1%; Query Match ORIGIN

Gaps ;; Indels 56; Mismatches 169; Conservative Best Local Similarity Matches

1;

1982 ACYTGYTGNCCNWSNARNARNGGNWSRTTYTCNCCDATNGGRCANWSRCARAADATNCKN 1923 113 acctgctgcccactgaggagggggctattctcaccaatgggacaagagcagaagatgcgg 172 = 쇰 გ

1922 GGNARNCKNARCCARTGNWSNWSNWSRTGNGGNARYTGNGGNACNWSRAARTCYTGYTTC 1863 173 ggtagacgcagtgactgctgctatgtggcaactggggtacggagaagtcttgcttc 232 염 g, 233 ataagtctgcgcctatatatcagagatgcaaggaccacagccatcaacaccagcaagatg 292 g

1862 ATHARNCKNCKNCKRTADATHARNWSNGCNARNACHACNGCCATHARNACHARNARDATH 1803

293 cccacqatcaqcqqaacctgcccaaqqcctgcttcttqaccaqqcatgataaqctqqqtg 352 g g

1802 CCNACDATNARNGGNACYTGNCCNARNCCNGCYTCYTGNCCNGGCATDATNARYTGNGTN 1743 cttgaccactgccaggctnttggtatcagccagagacacattgaggcagtatgtccccga 412 353 ç,

1742 - WSNACNACNGCNARNWSRTTNGTRTCNGCNARNWSNACRTTNARRCARTANGTNCCNWS 1684 გ 셤

gccaccettcagtatetg 413 요

1683 NCCNCCYTTNARDATYTG 1666

g

LT 13 HS118284 standard; RNA; EST; 430

Bb.

RESULT
ID HS
AC N2
DT 29
DT 29
DE YX
DE A4
KW ES

29-DEC-1995 (Rel. 46, Created)
29-DEC-1995 (Rel. 46, Last updated, Version 1)
yx67c12.81 Homo sapiens cDNA clone 266806 3' similar to SP:A41234
A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR - ;.

Aug 27 19:12

9

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Male. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. ä This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 1982 ACYTGYTGNCCNWSNARNARNGGNWSRTTYTCNCCDATNGGRCANWSRCARAADATNCKN 1923 233 ataagtctgcgcctatatatcagagatgcaaggaccacagccatcaacaccagcaagatg 292 113 acctgctgcccactgaggaggggctattctcaccaatgggacaagagcagaagatgcgg 172 173 ggtagacgcagccagtgactgctgctatgtggcaactggggtacggaagtcttgcttc 232 293 cccacgatcagcggaacctgcccaaggccttgcttcttgaccaggcatgataagctgggt 352 Gaps Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and NbHM vector=pT7T3D (Pharmacia) with a modified polylinker RI sites of a modified pT7T3 vector (Pharmacia). Library 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 <u>ب</u> Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 431; 1 others Indels 56; Mismatches 91; Score 877; DB 113; Pred. No. 3.75e-264; Washington University School of Medicine 95 t /organism="Homo sapiens" High quality sequence stops: 286 Source: IMAGE Consortium, LLNL Location/Qualifiers 105 c . 116 g The WashU-Merck EST Project Email: est@watson.wustl.edu /clone="266782" WashU-Merck EST Project /note="human" Query Match Best Local Similarity 52.8%; 1 (bases 1 to 431) 168; Conservative Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 41., 2431 NCBI gi: 1137261 1..431 Homo sapiens Wilson, R. 114 Albino. Bource ORGANISM BASE COUNT Matches REFERENCE AUTHORS FEATURES COMMENT ORIGIN g g 쇰 გ 염 g

School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 288 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., contact the IMAGE Consortium (info@image.llnl.gov) for further Contact: Wilson RK WashU-Merck EST Project Washington University Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; BP; 114 A; 107 C; 115 G; 93 T; 1 other; /organism="Homo sapiens" Location/Qualiflers /clone="266806" "The WashU-Merck EST Project"; information. NCBI gi: 1137268 /note="human" <1..>430 (human) Homo sapiens Sequence 430 Unpublished source mRNA 

Gaps ; Length 430; Indels 56; Mismatches 92; Score 948; DB 130; Pred. No. 6.28e-292; 12.4%; 53.1%; Best Local Similarity Query Match

1982 ACYTGYTGNCCNWSNARNARNGGNWSRTTYTCNCCDATNGGRCANWSRCARAADATNCKN 1923 113 acctgctgcccactgaggagggggtattctcaccaatgggacaagagcagaagatgcgg 172 Matches 169; Conservative 원 <u>ئ</u>

1922 GGNARNCKNARCCARTGNWSNWSNWSRTGNGGNARYTGNGGNACNWSRAARTCYTGYTTC 1863 173 ggtagacgcagccagtgactgctatgtggcaactggggtacggagaagtcttgcttc 232 셤 S,

1862 ATNARNCKNCKRTADATNARNWSNGCNARNACNACNGCCATNARNACNARNARDATN 1803 233 ataagtctgcgcctatatatcagagatgcaaggaccacagccatcaacaccagcaagatg 292 용 ტ

cccacgatcagcggaacctgcccaaggcctgcttcttgaccaggcatgataagctgggtg 352 293 a გ

413 gccaccettcagtatetg 430 

a g

1683 NCCNCCYTTNARDATYTG 1666

N23111 431 bp mRNA EST 28-yx67a12.s1 Homo sapiens cDNA clone 266782 3' similar A41234 MELANOCYTE-SPECIFIC PROTEIN PMEL-17 PRECURSOR N23111 g1137261 RESULT 14 DEFINITION ACCESSION

28-DEC-1995 similar to SP:A41234

human clone=266782 primer=m13 -40 forward library=Soares melanocyte

KEYWORDS SOURCE

								3;				
1744	412 1686				•	E	•		172 1923	232	292 1803	352
1802 CCNACDATNARNGGNACYTGNCCNARNCCN-GCYTCYTGNCCNGGCATDATNARYTGNGT	353 gctgaccacttgccaggctgttggtatcagccagagacacatttgaggcagtatginccc	413 gagccaccttcagtatt 430      :    ::  : 1685 WSNCCNCCYTINARDATY 1668	EBSULT 15  ID HS111256 standard; RNA; EST; 431 BP.  AC N23111;  DT 29-DEC-1995 (Rel. 46, Created)  DT 29-DEC-1995 (Rel. 46, Last updated, Version 1)  DE yx57a12.s1 Homo sapiens CDNA clone 266782 3' similar to SP:A41234 DE A41234 MELANOCYTE-SPECIFIC PROPEIN PMEL-17 PRECURSOR - ;		1-431 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., The WashU-Merck EST Project",		source 1431 /organism="Homo sapiens" /clone="266782" /note="human" <1431 Sequence 431 BP; 114 A; 105 C; 116 G; 95 T; 1 other;	Query Match 11.5%; Score 877; DB 129; Length 431; Best Local Similarity 52.8%; Pred. No. 3.75e-264; Matches 188; Conservative 56; Mismatches 91; Indels 3; Gaps	113 acctgctgcccactgaggaggggctattctcaccaatgggacaagagcagaagtgcgg	173 ggtagacgcagtgactgctgtgttgtggcaactggggtacggagagtcttgcttc	233 ataagtctgcgcctatatatcagagatgcaaggaccacagccatcaaccagcaagatg     :  :  :  :   :  :    :	293 cccacgatcagcggaacctgcccaaggccttgcttcttgaccaggcatgataagctgggt
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## US-08-231-565A-27 rst Aug 27 19 12

- CP 1802 CCNACDATNARNGGNACYTGNCCNARNCCN-GCYTCYTGNCCNGGCATDATNARYTGNGT 1744
- 413 gagccaccttcagtatt 430 || ||:||| |::||: 1685 WSNCCNCCYTTNARDATY 1668

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Сp

Search completed: Tue Aug 27 19:24:57 1996 Job time: 785 secs.

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            155 S MART OR GP100
L1
L2
           7055 S NUCLEIC ACID
           4343 S CDNA
L3
           8911 S L2 OR L3
L4
             14 S L1 AND L4
L5
              7 S L1(L)L4
L6
              0 S L1(P)L4
L7
              7 S L6
L8
=> d 1-7 cit
```

- 1. 5,494,891, Jan. 16, 1996, Selectin ligands; Laurence A. Lasky, et al. 530/387.3; 435/7.2; 530/350, 395 [IMAGE AVAILABLE]
- 2. 5,464,815, Nov. 7, 1995, Inhibition of heparin-binding; Steven Chamow, et al., 514/8; 424/85.2; 436/86, 87; 514/21; 530/412 [IMAGE AVAILABLE]
- 3. 5,269,025, Nov. 29, 1994, Recombinant fowlpox vaccine for protection against Marek's disease; Keyvan Nazerian, et al., 435/235.1; 424/186.1, 199.1, 229.1; 435/69.3, 172.3, 240.2; 530/350; 536/23.72; 935/9, 32, 34, 57, 63, 65, 70 [IMAGE AVAILABLE]
- 4. 5,318,890, Jun. 7, 1994, Assays for inhibitors of leukocyte adhesion; Steven Rosen, et al., 435/7.24, 7.1, 7.2, 7.92; 530/387.3 [IMAGE AVAILABLE]
- 5. 5,304,640, Apr. 19, 1994, DNA sequence encoding a selectin ligand; Laurence A. Lasky, et al., 536/23.5; 435/69.1, 172.3, 240.2, 320.1 [IMAGE AVAILABLE]
- 6. 5,242,829, Sep. 7, 1993, Recombinant pseudorabies virus; Dennis L. Panicali, et al., 435/320.1; 424/199.1, 229.1, 232.1; 435/69.1, 69.3, 1/2.3 [IMAGE AVAILABLE]
- 7. 5,141,922, Aug. 25, 1992, Biologically active proteins and a method for their use; Gwen G. Krivi, 514/12, 21; 530/324, 399 [IMAGE AVAILABLE]

=> d	his			
	(FILE	'USPA	T	' ENTERED AT 10:46:09 ON 27 AUG 96)
			Ε	KAWAKAMI, Y/IN
			Ε	ROSENBERG, S/IN
L1		24	S	E15,E14
L2		0	S	MELANONA(3A)ANTIGEN#(5A)(LYMPHOCYTE# OR LYMPHOKYTE#)
L3		3	S	MELANOMA(3A)ANTIGEN#(5A)(LYMPHOCYTE# OR LYMPHOKYTE#)
L4		7055	S	NUCLEIC ACID
L5		4343	S	CDNA
L6		8911	S	L4 OR L5
L7		0	S	L6 AND L3
L8		9	S	L1 AND L6
L9		0	S	L3 AND L8